GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 11, 2006, 22:15:38 ; Search time 209.448 Seconds
(without alignments)
4398.662 Million cell updates/sec

Title: US-10-632-342-8
Perfect score: 10489
Sequence: 1 MANFLLPRGTSSFRRFTRES.....HSEDLADFPPSPDRDRESIV 2015

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10489	100.0	2015	8	ADM34001	Adm34001 Human SCN
2	10487	99.9	2015	7	ADF56441	Adf56441 Human Nav
3	10484	99.9	2015	8	ADM33999	Adm33999 Human SCN
4	10484	99.9	2015	9	AEB22972	Aeb22972 Sodium ch
5	10478.5	99.9	2016	8	ADM33997	Adm33997 Human SCN
6	10478	99.9	2015	9	AEB22993	Aeb22993 Mutant hu
7	10478	99.9	2015	9	AEB22994	Aeb22994 Mutant hu
8	10473.5	99.9	2016	8	ADM33995	Adm33995 Human SCN
9	10473.5	99.9	2016	10	AEF90518	Aef90518 Human SCN
10	10471	99.8	2015	9	AEA78664	Aea78664 Human SCN
11	10432.5	99.5	2016	4	AAB82239	Aab82239 Human SCN
12	10432.5	99.5	2016	7	ADD44756	Add44756 Human Pro
13	10432.5	99.5	2016	7	ADE55106	Ade55106 Human Pro
14	10429.5	99.4	2016	4	AAB82245	Aab82245 Human SCN
15	10429.5	99.4	2016	4	AAB82241	Aab82241 Human SCN
16	10428.5	99.4	2016	4	AAB82244	Aab82244 Human SCN
17	10427.5	99.4	2016	4	AAB82240	Aab82240 Human SCN
18	10425.5	99.4	2016	4	AAB82243	Aab82243 Human SCN
19	10421.5	99.4	2016	2	AAW23994	Aaw23994 Human hH1
20	10416	99.3	2015	4	AAB82242	Aab82242 Human SCN
21	9767	93.1	2019	2	AAR67913	Aar67913 Cardiac s
22	9719	92.7	2020	2	AAR06584	Aar06584 Cardiac s
23	7659.5	73.0	1603	4	AAU19518	Aau19518 Human dia
24	6406.5	61.1	2000	8	ADP79541	Adp79541 Human sod
25	6394.5	61.0	2005	4	AAB99676	Aab99676 Human adu
26	6394.5	61.0	2005	9	ADY27148	Ady27148 Human SCN
27	6393.5	61.0	2005	9	ADY27149	Ady27149 Human SCN
28	6392.5	60.9	2005	5	ABB83627	Abb83627 Human GEF
29	6392.5	60.9	2005	7	ADB78604	Adb78604 Human sod
30	6391.5	60.9	2005	7	ADB78603	Adb78603 Human sod
31	6391.5	60.9	2005	7	ADB78605	Adb78605 Human sod
32	6391.5	60.9	2005	7	ADC46947	Adc46947 Human SCN
33	6391.5	60.9	2005	8	ADS52265	Ads52265 Human sod
34	6391.5	60.9	2005	9	ADY27151	Ady27151 Human SCN
35	6390.5	60.9	2005	9	ADY27150	Ady27150 Human SCN
36	6389.5	60.9	2005	4	AAB99677	Aab99677 Human neo
37	6387.5	60.9	2005	9	ADY27147	Ady27147 Human SCN
38	6377.5	60.8	2000	5	ABB06027	Abb06027 Human sod
39	6377.5	60.8	2000	8	ADK81762	Adk81762 Human Nav
40	6377.5	60.8	2000	8	ADP79545	Adp79545 Human sod
41	6377.5	60.8	2000	9	AEA44248	Aea44248 Human sod
42	6342.5	60.5	1979	9	AEA44245	Aea44245 Murine so
43	6329.5	60.3	2009	4	AAB99674	Aab99674 Human adu
44	6329.5	60.3	2009	7	ABR83180	Abr83180 Human SCN
45	6329.5	60.3	2009	7	ADE57563	Ade57563 Human Pro
46	6327.5	60.3	2009	7	ADE57561	Ade57561 Rat Prote
47	6327.5	60.3	2009	9	ADX26412	Adx26412 Novel cel
48	6324.5	60.3	2009	5	AAE20515	Aae20515 Human ion
49	6324.5	60.3	2009	5	ABB83626	Abb83626 Human GEF
50	6320.5	60.3	2009	8	ADS87512	Ads87512 Mutant SC
51	6319.5	60.2	2009	5	ABG69292	Abg69292 Human sod
52	6319	60.2	1998	7	ABR83184	Abr83184 Human SCN
53	6319	60.2	1998	9	ADX26269	Adx26269 Novel cel
54	6319	60.2	1998	9	AEB43184	Aeb43184 Human pot
55	6317.5	60.2	2009	8	ADS87505	Ads87505 Mutant SC
56	6316.5	60.2	2009	5	ABG69291	Abg69291 Human sod
57	6316.5	60.2	2009	5	ABG69290	Abg69290 Human sod
58	6316.5	60.2	2009	5	AAE16776	Aae16776 Human tra
59	6316.5	60.2	2009	7	ADB78598	Adb78598 Human sod
60	6316.5	60.2	2009	8	ADS87509	Ads87509 Mutant SC
61	6315.5	60.2	2009	8	ADS87515	Ads87515 Mutant SC
62	6315.5	60.2	2009	8	ADS87513	Ads87513 Mutant SC
63	6315.5	60.2	2009	8	ADS87532	Ads87532 Mutant SC
64	6315.5	60.2	2009	8	ADS87507	Ads87507 Mutant SC
65	6314.5	60.2	2009	7	ADB78593	Adb78593 Human sod
66	6314.5	60.2	2009	8	ADS87508	Ads87508 Mutant SC
67	6314.5	60.2	2009	8	ADS87511	Ads87511 Mutant SC
68	6314.5	60.2	2009	8	ADS87504	Ads87504 Mutant SC
69	6314.5	60.2	2009	8	ADS87530	Ads87530 Mutant SC
70	6314.5	60.2	2009	9	ADY27139	Ady27139 Human SCN
71	6314	60.2	1998	5	AAE20510	Aae20510 Human ion
72	6313.5	60.2	2009	7	ADB78595	Adb78595 Human sod
73	6313.5	60.2	2009	8	ADS87506	Ads87506 Mutant SC
74	6313.5	60.2	2009	9	ADY27142	Ady27142 Human SCN
75	6313.5	60.2	2009	9	ADY27140	Ady27140 Human SCN
76	6313.5	60.2	2009	9	ADY27144	Ady27144 Human SCN
77	6312.5	60.2	2009	5	ABG69293	Abg69293 Human sod
78	6312.5	60.2	2009	7	ADB78599	Adb78599 Human sod
79	6312.5	60.2	2009	8	ADS87514	Ads87514 Mutant SC
80	6311.5	60.2	2009	8	ADS87503	Ads87503 Mutant SC
81	6310.5	60.2	2009	5	ABG69289	Abg69289 Human sod
82	6310.5	60.2	2009	8	ADS87502	Ads87502 Mutant SC
83	6310.5	60.2	2009	8	ADS87531	Ads87531 Mutant SC
84	6310.5	60.2	2009	9	ADY27141	Ady27141 Human SCN
85	6309.5	60.2	2009	7	ADB78594	Adb78594 Human sod
86	6308.5	60.1	1950	7	ADB78607	Adb78607 Human sod
87	6308	60.1	1951	8	ADP79543	Adp79543 Human sod
88	6307.5	60.1	2009	8	ADS87510	Ads87510 Mutant SC
89	6300.5	60.1	1999	5	ABB06026	Abb06026 Human sod
90	6300.5	60.1	1999	8	ADU78366	Adu78366 Human vol
91	6289	60.0	1951	4	AAB99678	Aab99678 Human adu
92	6287	59.9	1973	5	AAE20516	Aae20516 Human ion
93	6285.5	59.9	1981	7	ABR83185	Abr83185 Human SCN
94	6283	59.9	1951	4	AAB99679	Aab99679 Human neo
95	6281	59.9	1951	8	ADL06576	Adl06576 Human tum
96	6281	59.9	1951	9	AEA44250	Aea44250 Human SCN

97	6276.5	59.8	1962	5	AAE20511	Aae20511 Human ion
98	6272.5	59.8	1951	7	ADE59628	Ade59628 Rat Prote
99	6272.5	59.8	1951	9	AEA44252	Aea44252 Rat sodiu
100	6257.5	59.7	1956	4	AAG65785	Aag65785 Human SNS
101	6257.5	59.7	1956	4	AAB61996	Aab61996 Human per
102	6257.5	59.7	1956	6	ABG76193	Abg76193 Human vol
103	6257.5	59.7	1956	6	ABP72253	Abp72253 Human PN3
104	6257.5	59.7	1956	6	ADA50152	Ada50152 Human per
105	6257.5	59.7	1956	7	ADJ68903	Adj68903 Human hea
106	6257.5	59.7	1956	8	ADF08471	Adf08471 Human Nav
107	6257.5	59.7	1956	8	ADU21150	Adu21150 Human sod
108	6257.5	59.7	1956	9	ADX26252	Adx26252 Novel cel
109	6257.5	59.7	1956	9	AEB90786	Aeb90786 Human per
110	6253.5	59.6	1956	8	ADU21152	Adu21152 Human sod
111	6251.5	59.6	1956	6	ABG75945	Abg75945 Human per
112	6245	59.5	1984	7	ADE54547	Ade54547 Rat Prote
113	6245	59.5	1984	7	ADE54551	Ade54551 Rat Prote
114	6245	59.5	1984	7	ADE63027	Ade63027 Rat Prote
115	6213.5	59.2	1977	8	ADE77202	Ade77202 Human pro
116	6213.5	59.2	1977	8	ADL13028	Adl13028 Human ste
117	6213.5	59.2	1977	9	AEB86379	Aeb86379 Amino aci
118	6213.5	59.2	1978	7	ADE54553	Ade54553 Human Pro
119	6213.5	59.2	1978	7	ADE54549	Ade54549 Human Pro
120	6212.5	59.2	1977	9	AEB86346	Aeb86346 Amino aci
121	6212.5	59.2	1977	9	AEB86347	Aeb86347 Amino aci
122	6212.5	59.2	1977	9	AEB86343	Aeb86343 Amino aci
123	6212.5	59.2	1977	9	AEB86348	Aeb86348 Amino aci
124	6210.5	59.2	1977	9	AEB86345	Aeb86345 Amino aci
125	6207.5	59.2	1977	2	AAR99641	Aar99641 Periphera
126	6206	59.2	1978	2	AAW69361	Aaw69361 Tetrodoto
127	6205.5	59.2	1977	9	AEB86344	Aeb86344 Amino aci
128	6198	59.1	1978	9	ADX26338	Adx26338 Novel cel
129	6197	59.1	1980	9	ADZ88372	Adz88372 Human SCN
130	6197	59.1	1988	2	AAW69362	Aaw69362 Tetrodoto
131	6194	59.1	1980	7	ADB78600	Adb78600 Human sod
132	6194	59.1	1984	2	AAR99639	Aar99639 Periphera
133	6189	59.0	1980	7	ADB78606	Adb78606 Human sod
134	6186	59.0	1989	2	AAR92317	Aar92317 Periphera
135	6178	58.9	1942	8	ADS87534	Ads87534 Mutant SC
136	6140	58.5	1980	3	AAB23563	Aab23563 Human sod
137	6140	58.5	1980	5	AAO14927	Aao14927 Human sod
138	6138.5	58.5	1962	2	AAY17250	Aay17250 NaNG poly
139	6110.5	58.3	1942	8	ADU21164	Adu21164 Guinea pi
140	6103.5	58.2	1957	6	ADA50156	Ada50156 Rat perip
141	6100	58.2	1956	4	AAG65783	Aag65783 Rat SNS1
142	6100	58.2	1956	4	AAB61995	Aab61995 Rat perip
143	6100	58.2	1956	6	ADA50153	Ada50153 Rat perip
144	6100	58.2	1956	8	ADU21165	Adu21165 Rat sodiu
145	6100	58.2	1956	9	AEB90788	Aeb90788 Rat perip
146	6088.5	58.0	1957	2	AAW21740	Aaw21740 Variant r
147	6087.5	58.0	1957	6	ABG76191	Abg76191 Rat volta
148	6087.5	58.0	1957	7	ADD44754	Add44754 Rat Prote
149	6087.5	58.0	1957	8	ADF08469	Adf08469 Rat Nav 1
150	6087.5	58.0	1957	8	ADU21148	Adu21148 Rat sodiu
151	6087.5	58.0	1957	9	ADX26396	Adx26396 Novel cel
152	6086.5	58.0	1957	2	AAW21737	Aaw21737 Wild type
153	6078	57.9	1891	9	ADY27145	Ady27145 Human SCN
154	6078	57.9	1958	4	AAG65784	Aag65784 Mouse SNS
155	6078	57.9	1958	9	ADX26323	Adx26323 Novel cel
156	6066.5	57.8	1836	7	ADE57388	Ade57388 Human Pro
157	6066.5	57.8	1836	7	ADE59630	Ade59630 Human Pro
158	6066.5	57.8	1836	7	ADE63029	Ade63029 Human Pro
159	6060.5	57.8	1836	8	ADQ17412	Adq17412 Human sof
160	6059.5	57.8	1836	9	AEF53825	Aef53825 Human vol
161	6049.5	57.7	1957	6	ADA50155	Ada50155 Rat perip
162	6049	57.7	1976	7	ADE57386	Ade57386 Rat Prote
163	6046	57.6	1956	6	ABG75944	Abg75944 Rat perip
164	6046	57.6	1956	6	ADA50144	Ada50144 Rat perip
165	6046	57.6	1956	9	AEB90778	Aeb90778 Rat perip
166	6043	57.6	2132	2	AAW21739	Aaw21739 Variant r
167	6012	57.3	1989	2	AAR99640	Aar99640 Periphera
168	5876	56.0	1855	7	ADB78597	Adb78597 Human sod
169	5644	53.8	1795	7	ADB78596	Adb78596 Human sod
170	5566.5	53.1	1835	2	AAR92316	Aar92316 Periphera
171	5456	52.0	1107	6	ABR41495	Abr41495 Human DIT
172	5293	50.5	1726	9	ADZ88370	Adz88370 Human SCN
173	4811	45.9	1765	2	AAY06597	Aay06597 Mouse sod
174	4811	45.9	1765	4	AAB20124	Aab20124 Mouse sod
175	4811	45.9	1765	7	ADD32196	Add32196 Mouse Na
176	4811	45.9	1765	9	ADX26317	Adx26317 Novel cel
177	4729	45.1	1791	5	AAO14925	Aao14925 Human sod
178	4729	45.1	1791	9	ADX26245	Adx26245 Novel cel
179	4729	45.1	1825	9	AED29799	Aed29799 Human SCN
180	4728	45.1	1765	7	ADD32192	Add32192 Rat Na v
181	4728	45.1	1765	7	ADD32210	Add32210 Rat Na v
182	4728	45.1	1765	7	ADE55104	Ade55104 Rat Prote
183	4728	45.1	1765	9	ADX26389	Adx26389 Novel cel
184	4724	45.0	1765	2	AAY16572	Aay16572 Type 5 so
185	4724	45.0	1791	4	AAB20121	Aab20121 Human sod
186	4724	45.0	1791	7	ADD32194	Add32194 Human Na
187	4720	45.0	1765	2	AAY06596	Aay06596 Rat sodiu
188	4720	45.0	1765	4	AAB20122	Aab20122 Rat sodiu
189	4720	45.0	1765	4	AAB20123	Aab20123 Rat sodiu
190	4719	45.0	1765	2	AAY41668	Aay41668 Rat senso
191	4711	44.9	1753	9	AED29797	Aed29797 Human SCN
192	4488.5	42.8	1510	8	ADS87522	Ads87522 Mutant SC
193	4207.5	40.1	1453	5	AAE20517	Aae20517 Human ion
194	4197	40.0	1442	5	AAE20512	Aae20512 Human ion
195	4173.5	39.8	2131	4	ABB64743	Abb64743 Drosophil
196	4173.5	39.8	2131	8	ADI30141	Adi30141 Drosophil
197	4169.5	39.8	2131	8	ADI30146	Adi30146 Drosophil
198	4167	39.7	2105	2	AAW57772	Aaw57772 Musca dom
199	4167	39.7	2105	2	AAW89577	Aaw89577 Calcium p
200	4162	39.7	2104	2	AAW57773	Aaw57773 Musca dom

ALIGNMENTS

RESULT 1
ADM34001
ID ADM34001 standard; protein; 2015 AA.
XX
AC ADM34001;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human SCN5A variant 4 protein SEQ ID NO:8.
XX
KW human; cardiac sodium channel alpha subunit; SCN5A;
KW sodium voltage-gated channel; type V; alpha; mutation study;
KW sodium channel related disease.
XX
OS Homo sapiens.
XX
PN WO2004012668-A2.
XX
PD 12-FEB-2004.
XX
PF 01-AUG-2003; 2003WO-US024190.
XX
PR 02-AUG-2002; 2002US-0401018P.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Makielski JC, Ye B, Ackerman MJ;
XX
DR WPI; 2004-157000/15.
DR N-PSDB; ADM34000.
XX
PT New nucleic acid encoding sodium voltage-gated channel, type V, alpha
PT polypeptide variants, useful for studying mutations, and designing or
PT identifying new diagnostics and treatment strategies or agents for sodium
PT channel related diseases.
XX
PS Claim 17; SEQ ID NO 8; 111pp; English.

XX
CC The present sequence represents a variant of the human cardiac sodium
CC channel alpha subunit designated SCN5A (sodium voltage-gated channel,
CC type V, alpha) protein. The present invention describes an isolated
CC polynucleotide encoding an SCN5A polypeptide where the polynucleotide is
CC selected from the group: (1) a first polynucleotide that encodes an SCN5A
CC polypeptide selected from the group consisting of: (i) a histidine,
CC threonine, leucine, arginine and glutamine at amino acid positions 558,
CC 559, 618, 1027 and 1077, respectively; (ii) an arginine, threonine,
CC leucine, arginine and glutamine at amino acid positions 558, 559, 618,
CC 1027 and 1077, respectively; (iii) a histidine, threonine, leucine and
CC arginine at amino acid positions 558, 559, 618 and 1027, respectively,
CC with the amino acid at amino acid position 1077 deleted; or (iv) an
CC arginine, threonine, leucine and arginine at amino acid positions 558,
CC 559, 618 and 1027, respectively, with the amino acid at amino acid
CC position 1077 deleted; (2) a second polynucleotide that is at least 80 %
CC identical to the first polynucleotide over the entire length of the first
CC polypeptide; (3) a third polynucleotide that encodes any of the SCN5A
CC polypeptides with a conservative substitution, deletion or rearrangement
CC at one or more non-critical amino acid position; and (4) a fourth
CC polynucleotide that is a complement of the first, second or third
CC polynucleotide. Also described: (1) a genetic construct comprising the
CC polynucleotide operably linked to a non-native expression control
CC sequence; (2) a cell comprising the polynucleotide; (3) an isolated
CC polypeptide encoded by the polynucleotide; (4) an antibody that
CC specifically binds to the polypeptide; (5) identifying an agent that can
CC alter the activity of a sodium channel; (6) identifying an agent that can
CC alter the expression of a sodium channel; (7) determining whether a
CC biological sample or a preparation derived from the biological sample
CC contains the polypeptide; (8) determining whether a mutation on a sodium
CC channel is associated with a disease; and (9) determining whether a human
CC or non-human subject is at risk for Long QT syndrome. The SCN5A
CC polynucleotides and polypeptides are useful for studying mutations, and
CC designing or identifying new diagnostics and treatment strategies or
CC agents for sodium channel related diseases or conditions.
XX
SQ Sequence 2015 AA;

Query Match 100.0%; Score 10489; DB 8; Length 2015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320

Qy       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
```

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Qy       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980

Qy       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
```

RESULT 2
ADF56441
ID ADF56441 standard; protein; 2015 AA.
XX
AC ADF56441;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human Nav1.5 sodium channel alpha subunit SCN5A hH1b.
XX
KW cardiant; antiarrhythmic; sodium channel blocker;
KW sodium channel activator; SCN5A channel blocker; SCN5A channel activator;
KW sodium channel subunit hH1b; hH1b; SCN5A; Long QT syndrome;
KW sodium channel; cardiac arrhythmia; heart disorder;
KW human Nav1.5 doaium channel alpha subunit SCN5A.
XX
OS Homo sapiens.
XX
PN US2003157600-A1.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2002; 2002US-00077054.
XX
PR 12-FEB-2002; 2002US-00077054.
XX
PA (MAKI/) MAKIELSKI J C.
PA (YEBB/) YE B.
XX
PI Makielski JC, Ye B;
XX
DR WPI; 2003-688984/65.
DR N-PSDB; ADF56440.
XX
PT New sodium channel subunit hH1b polypeptide, useful for screening for
PT compounds which alter sodium channel activity for treating cardiac
PT arrhythmia and other sodium channel related cardiac conditions.
XX
PS Claim 1; SEQ ID NO 2; 24pp; English.
XX

CC The invention describes an isolated sodium channel subunit hH1b
CC polypeptide (I) comprising a fully defined 2015 amino acid sequence as
CC given in the specification optionally, carrying a conservative
CC substitution, deletion or rearrangement at one or more non-critical amino
CC acid position. Detecting the presence of the hH1b SCN5A gene is useful
CC for determining if a (non-)human subject is at risk for Long QT syndrome.
CC Agents screened that increase or decrease sodium channel activity are
CC useful for treating cardiac arrhythmia and other sodium channel related
CC heart disorders. This is the amino acid sequence of human Nav1.5 doaium
CC channel alpha subunit SCN5A.
XX
SQ Sequence 2015 AA;

Query Match 99.9%; Score 10487; DB 7; Length 2015;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2014; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHILRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
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Qy       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
Db      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy      1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
Db      1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy      1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
Db      1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy      1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
Db      1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy      1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
Db      1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320

Qy      1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
Db      1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy      1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
Db      1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy      1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500
Db      1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy      1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
Db      1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560

Qy      1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
Db      1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy      1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
Db      1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy      1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
Db      1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy      1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
Db      1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy      1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
Db      1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy      1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
Db      1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy      1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
Db      1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980

Qy      1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db      1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
```

RESULT 3
ADM33999
ID ADM33999 standard; protein; 2015 AA.
XX
AC ADM33999;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human SCN5A variant 3 protein SEQ ID NO:6.
XX
KW human; cardiac sodium channel alpha subunit; SCN5A;
KW sodium voltage-gated channel; type V; alpha; mutation study;
KW sodium channel related disease.
XX
OS Homo sapiens.
XX
PN WO2004012668-A2.
XX
PD 12-FEB-2004.
XX
PF 01-AUG-2003; 2003WO-US024190.
XX
PR 02-AUG-2002; 2002US-0401018P.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Makielski JC, Ye B, Ackerman MJ;
XX
DR WPI; 2004-157000/15.
DR N-PSDB; ADM33998.
XX
PT New nucleic acid encoding sodium voltage-gated channel, type V, alpha
PT polypeptide variants, useful for studying mutations, and designing or
PT identifying new diagnostics and treatment strategies or agents for sodium
PT channel related diseases.
XX
PS Claim 14; SEQ ID NO 6; 111pp; English.
XX
CC The present sequence represents a variant of the human cardiac sodium
CC channel alpha subunit designated SCN5A (sodium voltage-gated channel,
CC type V, alpha) protein. The present invention describes an isolated
CC polynucleotide encoding an SCN5A polypeptide where the polynucleotide is
CC selected from the group: (1) a first polynucleotide that encodes an SCN5A
CC polypeptide selected from the group consisting of: (i) a histidine,
CC threonine, leucine, arginine and glutamine at amino acid positions 558,
CC 559, 618, 1027 and 1077, respectively; (ii) an arginine, threonine,
CC leucine, arginine and glutamine at amino acid positions 558, 559, 618,
CC 1027 and 1077, respectively; (iii) a histidine, threonine, leucine and
CC arginine at amino acid positions 558, 559, 618 and 1027, respectively,
CC with the amino acid at amino acid position 1077 deleted; or (iv) an
CC arginine, threonine, leucine and arginine at amino acid positions 558,
CC 559, 618 and 1027, respectively, with the amino acid at amino acid
CC position 1077 deleted; (2) a second polynucleotide that is at least 80 %
CC identical to the first polynucleotide over the entire length of the first
CC polypeptide; (3) a third polynucleotide that encodes any of the SCN5A
CC polypeptides with a conservative substitution, deletion or rearrangement
CC at one or more non-critical amino acid position; and (4) a fourth
CC polynucleotide that is a complement of the first, second or third
CC polynucleotide. Also described: (1) a genetic construct comprising the
CC polynucleotide operably linked to a non-native expression control
CC sequence; (2) a cell comprising the polynucleotide; (3) an isolated
CC polypeptide encoded by the polynucleotide; (4) an antibody that
CC specifically binds to the polypeptide; (5) identifying an agent that can
CC alter the activity of a sodium channel; (6) identifying an agent that can
CC alter the expression of a sodium channel; (7) determining whether a

CC biological sample or a preparation derived from the biological sample
CC contains the polypeptide; (8) determining whether a mutation on a sodium
CC channel is associated with a disease; and (9) determining whether a human
CC or non-human subject is at risk for Long QT syndrome. The SCN5A
CC polynucleotides and polypeptides are useful for studying mutations, and
CC designing or identifying new diagnostics and treatment strategies or
CC agents for sodium channel related diseases or conditions.
XX
SQ Sequence 2015 AA;

Query Match 99.9%; Score 10484; DB 8; Length 2015;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320

Qy       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560

Qy       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
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Qy       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015


RESULT 4
AEB22972
ID   AEB22972 standard; protein; 2015 AA.
XX
AC   AEB22972;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Sodium channel alpha subunit human SCN5A gene derived protein.
XX
KW   SCN5A; sodium channel; Brugada syndrome; heart arrhythmia;
KW   antiarrhythmic; selectable marker; ventricular fibrillation.
XX
OS   Homo sapiens.
XX
PN   JP2005192413-A.
XX
PD   21-JUL-2005.
XX
PF   26-DEC-2003; 2003JP-00435234.
XX
PR   26-DEC-2003; 2003JP-00435234.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
PI   Matsunaga A;
XX
DR   WPI; 2005-501993/51.
XX
PT   Novel SCN5A gene of sodium channel alpha subunit, with mutations in which
PT   glycine being substituted by serine, and serine being substituted by
PT   leucine, at specific positions, useful as marker for diagnosing Brugada
PT   syndrome.
XX
PS   Disclosure; SEQ ID NO 1; 30pp; Japanese.
XX
CC   The invention relates to an novel SCN5A gene of a sodium channel alpha
CC   subunit. The novel SCN5A gene comprises the mutation G292S between the
CC   fifth and sixth membrane passing-through subunits of the first domain;
CC   and/or the mutation S835L of the intracellular loop between the fourth
CC   and fifth membrane passing-through subunits of the second domain. The
CC   novel SCN5A gene can be used as a Brugada syndrome marker, for diagnosing
CC   Brugada syndrome. Brugada syndrome causes idiopathic ventricular
CC   fibrillation, thus the gene/marker allow for the prevention or treatment
CC   of the syndrome. This sequence represents the protein of the wild-type
CC   human SCN5A gene of the invention.
XX
SQ   Sequence 2015 AA;

  Query Match             99.9%;  Score 10484;  DB 9;  Length 2015;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2014;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
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Qy       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560

Qy       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980

Qy       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
```

RESULT 5
ADM33997
ID ADM33997 standard; protein; 2016 AA.
XX
AC ADM33997;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human SCN5A variant 2 protein SEQ ID NO:4.
XX
KW human; cardiac sodium channel alpha subunit; SCN5A;
KW sodium voltage-gated channel; type V; alpha; mutation study;
KW sodium channel related disease.
XX
OS Homo sapiens.
XX
PN WO2004012668-A2.
XX
PD 12-FEB-2004.
XX
PF 01-AUG-2003; 2003WO-US024190.
XX
PR 02-AUG-2002; 2002US-0401018P.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Makielski JC, Ye B, Ackerman MJ;
XX
DR WPI; 2004-157000/15.
DR N-PSDB; ADM33996.
XX
PT New nucleic acid encoding sodium voltage-gated channel, type V, alpha
PT polypeptide variants, useful for studying mutations, and designing or
PT identifying new diagnostics and treatment strategies or agents for sodium
PT channel related diseases.
XX
PS Claim 11; SEQ ID NO 4; 111pp; English.
XX
CC The present sequence represents a variant of the human cardiac sodium
CC channel alpha subunit designated SCN5A (sodium voltage-gated channel,
CC type V, alpha) protein. The present invention describes an isolated
CC polynucleotide encoding an SCN5A polypeptide where the polynucleotide is
CC selected from the group: (1) a first polynucleotide that encodes an SCN5A
CC polypeptide selected from the group consisting of: (i) a histidine,
CC threonine, leucine, arginine and glutamine at amino acid positions 558,
CC 559, 618, 1027 and 1077, respectively; (ii) an arginine, threonine,
CC leucine, arginine and glutamine at amino acid positions 558, 559, 618,
CC 1027 and 1077, respectively; (iii) a histidine, threonine, leucine and
CC arginine at amino acid positions 558, 559, 618 and 1027, respectively,
CC with the amino acid at amino acid position 1077 deleted; or (iv) an
CC arginine, threonine, leucine and arginine at amino acid positions 558,
CC 559, 618 and 1027, respectively, with the amino acid at amino acid
CC position 1077 deleted; (2) a second polynucleotide that is at least 80 %
CC identical to the first polynucleotide over the entire length of the first
CC polypeptide; (3) a third polynucleotide that encodes any of the SCN5A
CC polypeptides with a conservative substitution, deletion or rearrangement
CC at one or more non-critical amino acid position; and (4) a fourth
CC polynucleotide that is a complement of the first, second or third
CC polynucleotide. Also described: (1) a genetic construct comprising the
CC polynucleotide operably linked to a non-native expression control
CC sequence; (2) a cell comprising the polynucleotide; (3) an isolated
CC polypeptide encoded by the polynucleotide; (4) an antibody that
CC specifically binds to the polypeptide; (5) identifying an agent that can
CC alter the activity of a sodium channel; (6) identifying an agent that can
CC alter the expression of a sodium channel; (7) determining whether a
CC biological sample or a preparation derived from the biological sample
CC contains the polypeptide; (8) determining whether a mutation on a sodium
CC channel is associated with a disease; and (9) determining whether a human
CC or non-human subject is at risk for Long QT syndrome. The SCN5A
CC polynucleotides and polypeptides are useful for studying mutations, and
CC designing or identifying new diagnostics and treatment strategies or
CC agents for sodium channel related diseases or conditions.
XX
SQ Sequence 2016 AA;

Query Match 99.9%; Score 10478.5; DB 8; Length 2016;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2015; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
              |||||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
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RESULT 6
AEB22993
ID AEB22993 standard; protein; 2015 AA.
XX
AC AEB22993;
XX
DT 22-SEP-2005 (first entry)
XX
DE Mutant human SCN5A protein, S835L.
XX
KW SCN5A; sodium channel; Brugada syndrome; heart arrhythmia;
KW antiarrhythmic; selectable marker; ventricular fibrillation; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Misc-difference 835
FT   /note= "The wild-type Ser residue has been substituted
FT   with Leu"
XX
PN JP2005192413-A.
XX
PD 21-JUL-2005.
XX
PF 26-DEC-2003; 2003JP-00435234.
XX

PR 26-DEC-2003; 2003JP-00435234.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
PI Matsunaga A;
XX
DR WPI; 2005-501993/51.
XX
PT Novel SCN5A gene of sodium channel alpha subunit, with mutations in which
PT glycine being substituted by serine, and serine being substituted by
PT leucine, at specific positions, useful as marker for diagnosing Brugada
PT syndrome.
XX
PS Claim 1; Page; 30pp; Japanese.
XX
CC The invention relates to an novel SCN5A gene of a sodium channel alpha
CC subunit. The novel SCN5A gene comprises the mutation G292S between the
CC fifth and sixth membrane passing-through subunits of the first domain;
CC and/or the mutation S835L of the intracellular loop between the fourth
CC and fifth membrane passing-through subunits of the second domain. The
CC novel SCN5A gene can be used as a Brugada syndrome marker, for diagnosing
CC Brugada syndrome. Brugada syndrome causes idiopathic ventricular
CC fibrillation, thus the gene/marker allow for the prevention or treatment
CC of the syndrome. This sequence represents the S835L mutant protein of the
CC human SCN5A gene of the invention.
XX
SQ Sequence 2015 AA;

Query Match 99.9%; Score 10478; DB 9; Length 2015;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNLVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320

Qy       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560

Qy       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980

Qy       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
```

RESULT 7
AEB22994
ID AEB22994 standard; protein; 2015 AA.
XX
AC AEB22994;
XX
DT 22-SEP-2005 (first entry)
XX
DE Mutant human SCN5A protein, G292S.
XX
KW SCN5A; sodium channel; Brugada syndrome; heart arrhythmia;
KW antiarrhythmic; selectable marker; ventricular fibrillation; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 292
FT /note= "The wild-type Gly residue has been substituted
FT with Ser"
XX
PN JP2005192413-A.
XX
PD 21-JUL-2005.
XX
PF 26-DEC-2003; 2003JP-00435234.
XX
PR 26-DEC-2003; 2003JP-00435234.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
PI Matsunaga A;
XX
DR WPI; 2005-501993/51.
XX
PT Novel SCN5A gene of sodium channel alpha subunit, with mutations in which
PT glycine being substituted by serine, and serine being substituted by
PT leucine, at specific positions, useful as marker for diagnosing Brugada
PT syndrome.
XX
PS Claim 1; Page; 30pp; Japanese.
XX
CC The invention relates to an novel SCN5A gene of a sodium channel alpha
CC subunit. The novel SCN5A gene comprises the mutation G292S between the
CC fifth and sixth membrane passing-through subunits of the first domain;
CC and/or the mutation S835L of the intracellular loop between the fourth
CC and fifth membrane passing-through subunits of the second domain. The
CC novel SCN5A gene can be used as a Brugada syndrome marker, for diagnosing
CC Brugada syndrome. Brugada syndrome causes idiopathic ventricular
CC fibrillation, thus the gene/marker allow for the prevention or treatment
CC of the syndrome. This sequence represents the G292S mutant protein of the
CC human SCN5A gene of the invention.
XX
SQ Sequence 2015 AA;

Query Match 99.9%; Score 10478; DB 9; Length 2015;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNSSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
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Qy       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy      1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy      1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy      1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy      1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320

Qy      1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy      1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy      1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy      1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560

Qy      1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy      1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy      1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy      1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy      1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy      1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy      1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980

Qy      1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
            |||||||||||||||||||||||||||||||||||||
Db      1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
```

```
RESULT 8
ADM33995
ID   ADM33995 standard; protein; 2016 AA.
XX
AC   ADM33995;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human SCN5A variant 1 protein SEQ ID NO:2.
XX
KW   human; cardiac sodium channel alpha subunit; SCN5A;
KW   sodium voltage-gated channel; type V; alpha; mutation study;
KW   sodium channel related disease.
XX
OS   Homo sapiens.
XX
PN   WO2004012668-A2.
XX
PD   12-FEB-2004.
XX
PF   01-AUG-2003; 2003WO-US024190.
XX
PR   02-AUG-2002; 2002US-0401018P.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Makielski JC,  Ye B,  Ackerman MJ;
XX
DR   WPI; 2004-157000/15.
DR   N-PSDB; ADM33994.
XX
PT   New nucleic acid encoding sodium voltage-gated channel, type V, alpha
PT   polypeptide variants, useful for studying mutations, and designing or
PT   identifying new diagnostics and treatment strategies or agents for sodium
PT   channel related diseases.
XX
PS   Claim 8; SEQ ID NO 2; 111pp; English.
XX
CC   The present sequence represents a variant of the human cardiac sodium
CC   channel alpha subunit designated SCN5A (sodium voltage-gated channel,
CC   type V, alpha) protein. The present invention describes an isolated
CC   polynucleotide encoding an SCN5A polypeptide where the polynucleotide is
CC   selected from the group: (1) a first polynucleotide that encodes an SCN5A
CC   polypeptide selected from the group consisting of: (i) a histidine,
CC   threonine, leucine, arginine and glutamine at amino acid positions 558,
CC   559, 618, 1027 and 1077, respectively; (ii) an arginine, threonine,
CC   leucine, arginine and glutamine at amino acid positions 558, 559, 618,
CC   1027 and 1077, respectively; (iii) a histidine, threonine, leucine and
CC   arginine at amino acid positions 558, 559, 618 and 1027, respectively,
CC   with the amino acid at amino acid position 1077 deleted; or (iv) an
CC   arginine, threonine, leucine and arginine at amino acid positions 558,
CC   559, 618 and 1027, respectively, with the amino acid at amino acid
CC   position 1077 deleted; (2) a second polynucleotide that is at least 80 %
CC   identical to the first polynucleotide over the entire length of the first
CC   polypeptide; (3) a third polynucleotide that encodes any of the SCN5A
CC   polypeptides with a conservative substitution, deletion or rearrangement
CC   at one or more non-critical amino acid position; and (4) a fourth
CC   polynucleotide that is a complement of the first, second or third
CC   polynucleotide. Also described: (1) a genetic construct comprising the
CC   polynucleotide operably linked to a non-native expression control
CC   sequence; (2) a cell comprising the polynucleotide; (3) an isolated
CC   polypeptide encoded by the polynucleotide; (4) an antibody that
CC   specifically binds to the polypeptide; (5) identifying an agent that can
CC   alter the activity of a sodium channel; (6) identifying an agent that can
CC   alter the expression of a sodium channel; (7) determining whether a
CC   biological sample or a preparation derived from the biological sample
CC   contains the polypeptide; (8) determining whether a mutation on a sodium
CC   channel is associated with a disease; and (9) determining whether a human
CC   or non-human subject is at risk for Long QT syndrome. The SCN5A
CC   polynucleotides and polypeptides are useful for studying mutations, and
CC   designing or identifying new diagnostics and treatment strategies or
CC   agents for sodium channel related diseases or conditions.
XX
```

SQ Sequence 2016 AA;

Query Match 99.9%; Score 10473.5; DB 8; Length 2016;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2014; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
              |||||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
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RESULT 9
AEF90518
ID AEF90518 standard; protein; 2016 AA.

XX
AC AEF90518;
XX
DT 20-APR-2006 (first entry)
XX
DE Human SCN5 splice variant 1 SEQ ID NO 68.
XX
KW antiarrhythmic; gene therapy; screening; diagnosis; prognosis;
KW SNP detection; genetic marker; sudden infant death syndrome; SCN5;
KW voltage-gated sodium channel.
XX
OS Homo sapiens.
XX
PN WO2006019984-A2.
XX
PD 23-FEB-2006.
XX
PF 15-JUL-2005; 2005WO-US025099.
XX
PR 15-JUL-2004; 2004US-0588302P.
PR 14-APR-2005; 50US-05546987.
XX
PA (UYYA) UNIV YALE.
XX
PI Goldstein SAN, Bowers PN;
XX
DR WPI; 2006-174087/18.
DR N-PSDB; AEF90517.
XX
PT Testing a human individual for a marker for Sudden Infant Death Syndrome
PT comprises identifying a polymorphism in the cardiac sodium channel SCN5A
PT protein.
XX
PS Claim 3; SEQ ID NO 68; 88pp; English.
XX
CC The invention describes a method of testing a human individual for a
CC marker for Sudden Infant Death Syndrome (SIDS) comprising identifying a
CC polymorphism in a nucleic acid sample from the individual, where the
CC sample comprises both allelic copies of a nucleic acid encoding an SCN5A
CC polypeptide or copies of a protein encoded by the individual's SCN5A
CC nucleic acid. Also described are: a method of assessing a risk for SIDS
CC in a human individual; a method of identifying a human carrier of a
CC marker for SIDS; a kit, for testing a human infant or fetus for a marker,
CC assessing a risk, or for identifying a human carrier of a marker for a
CC marker for SIDS, the kit comprising: at least one reagent for identifying
CC an amino acid at a position corresponding to position 1103 in SEQ ID NO:
CC 68; and instructional material, where if the amino acid at a position
CC corresponding to position 1103 in SEQ ID NO: 2 is Y/Y, then the infant or
CC fetus has a marker for SIDS or is assessed to be at increased risk for
CC SIDS relative to an infant or fetus in which the amino acid at a position
CC corresponding to position 1103 in SEQ ID NO:68 is not Y/Y, or where if
CC the amino acid at a position corresponding to position 1103 in SEQ ID NO:
CC 68 is Y/- or Y/Y, then the human is identified as a carrier of a marker
CC for SIDS; a method of screening for SIDS in a human infant or fetus; a
CC method for diagnosing SIDS in an infant or fetus; and a method for
CC preventing SIDS in a human infant or fetus. The methods and kits are
CC useful for testing a human individual for a marker for SIDS, assessing a
CC risk for SIDS in a human individual, identifying a human carrier of a
CC marker for SIDS, and for screening and diagnosing SIDS in a human infant
CC or fetus. The method and composition are useful for preventing SIDS in a
CC human infant or fetus. This is the amino acid sequence of human SCN5
CC splice variant 1.
XX
SQ Sequence 2016 AA;

Query Match 99.9%; Score 10473.5; DB 10; Length 2016;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2014; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
                |||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016


RESULT 10
AEA78664
ID   AEA78664 standard; protein; 2015 AA.
XX
AC   AEA78664;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human SCN5A sodium channel subunit (wild-type), SEQ ID NO:3.
XX
KW   Diagnosis; cardiovascular disease; heart arrhythmia; long QT syndrome;
KW   short QT syndrome; Brugada syndrome; progressive conduction disease;
KW   cardiac arrest; sodium channel, voltage-gated, type V, alpha; SCN5A;
KW   single amino acid polymorphism; SAP.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 104
FT                   /note= "Optionally, Trp replaces wild-type Arg in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 179
FT                   /note= "Optionally, an in-frame stop codon replaces wild-
FT                   type Arg in a mutant SCN5A protein of the invention.
FT                   Mutation is associated with Brugada syndrome"
FT   Misc-difference 220
FT                   /note= "Optionally, Ile replaces wild-type Thr in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 232
FT                   /note= "Optionally, Ile replaces wild-type Val in
FT                   conjunction with the amino acid substitution L1307F in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 336
FT                   /note= "Optionally, Leu replaces wild-type Pro in
FT                   conjunction with the amino acid substitution I1659V in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 400
FT                   /note= "Optionally, Ala replaces wild-type Gly in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 446
FT                   /note= "Optionally, Lys replaces wild-type Glu in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 532
FT                   /note= "Optionally, Cys replaces wild-type Phe in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 735
FT                   /note= "Optionally, Val replaces wild-type Ala in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 851. .2015
FT                   /note= "Optionally, this seqment is replaced with the
FT                   variant C-terminus CSSLLWWACSSLARTTRS in a mutant SCN5A
FT                   protein of the invention. Mutation is associated with
FT                   Brugada syndrome and results from a 2 base insertion
FT                   between codons 850 and 851 (TG851 mutation)"
FT   Misc-difference 878
FT                   /note= "Optionally, Cys replaces wild-type Arg in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 886
FT                   /note= "Optionally, Pro replaces wild-type His in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 917
FT                   /note= "Optionally, Arg replaces wild-type Leu in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 1008
FT                   /note= "Optionally, Ser replaces wild-type Pro in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with progressive conduction disease"
FT   Misc-difference 1134
FT                   /note= "Optionally, Ile replaces wild-type Ser in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with long QT syndrome"
FT   Misc-difference 1307
FT                   /note= "Optionally, Phe replaces wild-type Leu in
FT                   conjunction with the amino acid substitution V232I in a
FT                   mutant SCN5A protein of the invention. Mutation is
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FT                   associated with Brugada syndrome"
FT   Misc-difference 1573. .1604
FT                   /note= "Optionally, this segment is deleted in a mutant
FT                   SCN5A protein of the invention. Mutation is associated
FT                   with Brugada syndrome and results from aberrant splicing
FT                   of exons 27 and 28"
FT   Misc-difference 1573
FT                   /note= "Optionally, Lys replaces wild-type Glu in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 1614
FT                   /note= "Optionally, an in-frame stop codon replaces wild-
FT                   type Tyr in a mutant SCN5A protein of the invention.
FT                   Mutation is associated with Brugada syndrome"
FT   Misc-difference 1659
FT                   /note= "Optionally, Val replaces wild-type Ile in
FT                   conjunction with the amino acid substitution P336L in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
FT   Misc-difference 1727
FT                   /note= "Optionally, Arg replaces wild-type Cys in a
FT                   mutant SCN5A protein of the invention. Mutation is
FT                   associated with Brugada syndrome"
XX
PN   US2005130190-A1.
XX
PD   16-JUN-2005.
XX
PF   23-AUG-2004; 2004US-00924375.
XX
PR   22-AUG-2003; 2003US-0497256P.
XX
PA   (ANTZ/) ANTZELEVITCH C.
PA   (BRUG/) BRUGADA R.
PA   (HONG/) HONG K.
XX
PI   Antzelevitch C,  Brugada R,  Hong K;
XX
DR   WPI; 2005-443796/45.
DR   N-PSDB; AEA78665.
XX
PT   Novel isolated mutant ion channel protein e.g. KCNH2 protein,
PT   corresponding to wild-type human KCNH2 protein, useful for diagnosing and
PT   screening drugs to treat long and short QT syndrome.
XX
PS   Claim 7; SEQ ID NO 3; 65pp; English.
XX
CC   The invention relates to mutants of the ion channel proteins KCNQ1
CC   (potassium voltage-gated channel, KQT-like subfamily, member 1;
CC   AEA78662), SCN5A (sodium channel, voltage-gated, type V, alpha; AEA78664)
CC   and KCNH2 (potassium voltage-gated channel, subfamily H, member 2, also
CC   known as HERG; AEA78666), and to mutant KCNQ1, SCN5A and KCNH2 nucleic
CC   acids. The invention also relates to vectors and host cells comprising
CC   mutant nucleic acids of the invention; nucleic acid probes which
CC   selectively hybridize to a mutant KCNQ1, SCN5A or KCNH2 nucleic acid but
CC   not to the corresponding wild-type polynucleotide; microarrays containing
CC   such probes; and antibodies immunospecific for mutant KCNQ1, SCN5A or
CC   KCNH2 proteins. The mutant proteins of the invention result from
CC   previously unknown mutations in the KCNQ1, SCN5A and KCNH2 genes and are
CC   involved in ion channel disruptions associated with diseases resulting in
CC   arrhythmias and/or sudden cardiac death (cardiac arrest) such as short QT
CC   syndrome, long QT syndrome, Brugada syndrome and progressive conduction
CC   disease. The novel KCNQ1 mutation, G189W (sic), is associated with long
CC   QT syndrome. Most of the novel SCN5A mutations are associated with
CC   Brugada syndrome; these mutations are R104W, R179stop, T220I, G400A,
CC   E446K, F532C, A735V, R878C, H886P, L917R, E1573K, Y1614stop, C1727R,
CC   V2332I+L1307F, P336L+I1659V, TG851 (a TG base insertion between codons
CC   850 and 851 of the coding sequence), and a deletion of E1573-G1604
CC   (resulting from an aberrant "splice of exons 27 and 28=4810+7 ins GGG").
CC   The other novel SCN5A mutations, P1008S and S1134I are respectively
CC   associated with progressive conduction disease and long QT syndrome.
CC   There are 4 novel mutations of KCNH2; one of these, N588K is associated
CC   with short QT syndrome, while the other three, R356H, W398stop and C764
CC   deletion (a deletion of cytosine from codon 764 of the coding sequence),
CC   are associated with long QT syndrome. The mutant ion channel proteins,
CC   polynucleotides, antibodies and probes are useful for diagnosing short QT
CC   syndrome, Brugada syndrome, progressive conduction disease or long QT
CC   syndrome. They can be used to determine an individual's susceptibility to
CC   sudden cardiac death, or to determine whether this is the cause of death
CC   for a deceased individual. The proteins and polynucleotides are also
CC   useful in screening for compounds useful in treating the above-mentioned
CC   diseases. The present sequence represents the wild-type human SCN5A
CC   protein.
XX
SQ   Sequence 2015 AA;

  Query Match             99.8%;  Score 10471;  DB 9;  Length 2015;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2012;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTAGESESHHASLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
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Qy       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080
Db      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQESQP 1080

Qy      1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140
Db      1081 VSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGST 1140

Qy      1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200
Db      1141 ADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYHI 1200

Qy      1201 VEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260
Db      1201 VEHSWFETFIIFMILLSSGALAFEDIYLEEWKTIKVLLEYADKMFTYVFVLEMLLKWVAY 1260

Qy      1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320
Db      1261 GFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGMR 1320

Qy      1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380
Db      1321 VVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNNK 1380

Qy      1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440
Db      1381 SQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQWE 1440

Qy      1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKLGGQDIFMTEEQKKYYNAMKKL 1500
Db      1441 YNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKLGGQDIFMTEEQKKYYNAMKKL 1500

Qy      1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560
Db      1501 GSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINILA 1560

Qy      1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620
Db      1561 KINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTL 1620

Qy      1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680
Db      1621 FRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFAY 1680

Qy      1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740
Db      1681 VKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRGD 1740

Qy      1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800
Db      1741 CGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEKF 1800

Qy      1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860
Db      1801 DPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKRV 1860

Qy      1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920
Db      1861 LGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSL 1920

Qy      1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980
Db      1921 KHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVT 1980

Qy      1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db      1981 RATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
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RESULT 11
AAB82239
ID AAB82239 standard; protein; 2016 AA.
XX
AC AAB82239;
XX
DT 21-JUN-2001 (first entry)
XX
DE Human SCN5A protein.
XX
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US021660.
XX
PR 09-AUG-1999; 99US-0147488P.
PR 17-MAR-2000; 2000US-0190057P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Splawski I;
XX
DR WPI; 2001-290564/30.
DR N-PSDB; AAF30825.
XX
PT New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT useful in diagostic/prognostic or drug screening methods, particularly in
PT mutational analyses for screening individuals with or at risk for long QT
PT syndrome.
XX
PS Claim 31; Page 69-75; 76pp; English.
XX
CC The present sequence is that of the protein encoded by the human SCN5A
CC gene. This gene is implicated in Romano-Ward syndrome, the autosomal
CC dominant form of Long QT syndrome (LQTS). Novel mutations have been
CC identified in the gene using single strand conformation polymorphism
CC analysis. These result in the following amino acid alterations: D1114N,
CC L1501V, delF1617, R1623L, E1784K and S1787N. Isolated human polypeptides
CC comprising such a mutation (see AAB82240-45) are claimed. Knowledge of
CC the mutations provides means for assessing a risk in a human subject for
CC LQTS, for diagnosing a mutation which causes LQTS, and for screening for
CC drugs useful in treating a human having a mutation in the SCN5A gene
XX
SQ Sequence 2016 AA;

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  Query Match             99.5%;  Score 10432.5;  DB 4;  Length 2016;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2006;  Conservative    2;  Mismatches    7;  Indels    1;  Gaps    1;

Qy         1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
Db         1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy        61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
Db        61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy       121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
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Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180
Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Db        541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
Db       1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080
Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
Db       1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140
Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200
Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260
Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320
Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380
Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440
Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500
Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560
Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620
Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680
Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740
Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800
Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860
Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920
Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980
Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
```

RESULT 12
ADD44756
ID ADD44756 standard; protein; 2016 AA.
XX
AC ADD44756;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q14524, SEQ ID NO 10185.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.

XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q14524.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2016 AA;

Query Match 99.5%; Score 10432.5; DB 7; Length 2016;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2006; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||  |||||  ||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
              ||||||:||||||||||||||||||||||||||||||||||||||||||||| |||| 
Db       1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
              |||| |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380
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Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
```

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RESULT 13
ADE55106
ID   ADE55106 standard; protein; 2016 AA.
XX
AC   ADE55106;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein NP_000326, SEQ ID NO 911.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; NP_000326.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2016 AA;
```

Query Match 99.5%; Score 10432.5; DB 7; Length 2016;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2006; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
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Qy       421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Db       421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy       481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Db       481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy       541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Db       541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy       601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Db       601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy       661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Db       661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy       721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Db       721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy       781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Db       781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db       961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
Db      1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy      1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
Db      1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy      1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
Db      1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy      1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
Db      1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy      1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
Db      1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy      1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
Db      1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy      1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
Db      1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy      1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
Db      1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy      1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
Db      1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy      1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFPSPT 1619
Db      1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFPSPT 1620

Qy      1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
Db      1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy      1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
Db      1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy      1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
Db      1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy      1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
Db      1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy      1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
Db      1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy      1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
Db      1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy      1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db      1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
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RESULT 14
AAB82245
ID AAB82245 standard; protein; 2016 AA.
XX
AC AAB82245;
XX
DT 21-JUN-2001 (first entry)
XX
DE Human SCN5A mutant S1787N.
XX
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US021660.
XX
PR 09-AUG-1999; 99US-0147488P.
PR 17-MAR-2000; 2000US-0190057P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Splawski I;
XX
DR WPI; 2001-290564/30.
XX
PT New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT useful in diagostic/prognostic or drug screening methods, particularly in
PT mutational analyses for screening individuals with or at risk for long QT
PT syndrome.
XX
PS Claim 31; Page; 76pp; English.

XX
CC The present sequence is that of the claimed S1787N mutant of the human
CC SCN5A protein. The mutant is encoded by an SCN5A mutant gene in which a
CC G/A mutation alters codon 1787 from AGT to AAT. Mutations of the SCN5A
CC gene are implicated in Romano-Ward syndrome, the autosomal dominant form
CC of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene
CC lead to the following amino acid alterations in the encoded protein:
CC D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the
CC mutations provides means for assessing a risk in a human subject for
CC LQTS, for diagnosing a mutation which causes LQTS, and for screening for
CC drugs useful in treating a human having a mutation in the SCN5A gene.
CC Note: The present sequence is not shown in the specification but is
CC derived from the KVLQT-1 sequence given in the Sequence Listing (see
CC AAB82220)
XX
SQ Sequence 2016 AA;

Query Match 99.4%; Score 10429.5; DB 4; Length 2016;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2005; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

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Qy    1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
Db    1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy   61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
Db   61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy  121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
Db  121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy  181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
Db  181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy  241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
Db  241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy  301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
Db  301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy  361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
Db  361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy  421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Db  421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy  481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Db  481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy  541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Db  541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy  601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Db  601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy  661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Db  661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy  721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Db  721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy  781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Db  781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy  841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db  841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy  901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db  901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy  961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db  961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy 1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
Db 1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy 1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
Db 1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy 1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
Db 1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy 1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
Db 1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy 1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
Db 1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy 1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
Db 1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy 1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
Db 1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy 1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
Db 1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy 1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
Db 1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy 1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
Db 1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy 1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
Db 1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy 1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
Db 1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy 1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
Db 1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLNEDDFDMFYEIWEK 1800

Qy 1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
Db 1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy 1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
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Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979

Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015

Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016


RESULT 15
AAB82241
ID   AAB82241 standard; protein; 2016 AA.
XX
AC   AAB82241;
XX
DT   21-JUN-2001  (first entry)
XX
DE   Human SCN5A mutant L1501V.
XX
KW   SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW   Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening;
KW   mutant; mutein.
XX
OS   Homo sapiens.
XX
PN   WO200124681-A2.
XX
PD   12-APR-2001.
XX
PF   09-AUG-2000; 2000WO-US021660.
XX
PR   09-AUG-1999;   99US-0147488P.
PR   17-MAR-2000; 2000US-0190057P.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Splawski I;
XX
DR   WPI; 2001-290564/30.
XX
PT   New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT   useful in diagostic/prognostic or drug screening methods, particularly in
PT   mutational analyses for screening individuals with or at risk for long QT
PT   syndrome.
XX
PS   Claim 31; Page; 76pp; English.
XX
CC   The present sequence is that of the claimed L1501V mutant of the human
CC   SCN5A protein. The mutant is encoded by an SCN5A mutant gene in which a
CC   C/G mutation alters codon 1501 from CTG to GTG. Mutations of the SCN5A
CC   gene are implicated in Romano-Ward syndrome, the autosomal dominant form
CC   of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene
CC   lead to the following amino acid alterations in the encoded protein:
CC   D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the
CC   mutations provides means for assessing a risk in a human subject for
CC   LQTS, for diagnosing a mutation which causes LQTS, and for screening for
CC   drugs useful in treating a human having a mutation in the SCN5A gene.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the KVLQT-1 sequence given in the Sequence Listing (see
CC   AAB82220)
XX
SQ   Sequence 2016 AA;

  Query Match             99.4%;  Score 10429.5;  DB 4;  Length 2016;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2005;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120

Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180

Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Db        541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Db        961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRPEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079

Db       1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139

Db       1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140
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Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 VGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             ||||||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
```

RESULT 16
AAB82244
ID AAB82244 standard; protein; 2016 AA.
XX
AC AAB82244;
XX
DT 21-JUN-2001 (first entry)
XX
DE Human SCN5A mutant E1784K.
XX
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US021660.
XX
PR 09-AUG-1999; 99US-0147488P.
PR 17-MAR-2000; 2000US-0190057P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Splawski I;
XX
DR WPI; 2001-290564/30.
XX
PT New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT useful in diagostic/prognostic or drug screening methods, particularly in
PT mutational analyses for screening individuals with or at risk for long QT
PT syndrome.
XX
PS Claim 31; Page; 76pp; English.
XX
CC The present sequence is that of the claimed E1784K mutant of the human
CC SCN5A protein. The mutant is encoded by an SCN5A mutant gene in which a
CC G/A mutation alters codon 1784 from GAG to AAG. Mutations of the SCN5A
CC gene are implicated in Romano-Ward syndrome, the autosomal dominant form
CC of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene
CC lead to the following amino acid alterations in the encoded protein:
CC D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the
CC mutations provides means for assessing a risk in a human subject for
CC LQTS, for diagnosing a mutation which causes LQTS, and for screening for
CC drugs useful in treating a human having a mutation in the SCN5A gene.
CC Note: The present sequence is not shown in the specification but is
CC derived from the KVLQT-1 sequence given in the Sequence Listing (see
CC AAB82220)
XX
SQ Sequence 2016 AA;

Query Match 99.4%; Score 10428.5; DB 4; Length 2016;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2005; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
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Qy       421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Db       421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy       481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Db       481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy       541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Db       541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy       601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Db       601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy       661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Db       661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy       721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Db       721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy       781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Db       781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db       961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
Db      1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy      1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
Db      1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy      1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
Db      1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy      1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
Db      1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy      1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
Db      1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy      1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
Db      1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy      1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
Db      1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy      1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
Db      1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy      1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
Db      1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy      1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
Db      1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy      1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
Db      1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy      1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
Db      1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy      1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
Db      1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTKPLSEDDFDMFYEIWEK 1800

Qy      1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
Db      1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy      1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
Db      1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy      1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
Db      1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy      1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db      1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
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RESULT 17
AAB82240
ID AAB82240 standard; protein; 2016 AA.
XX
AC AAB82240;
XX
DT 21-JUN-2001 (first entry)
XX
DE Human SCN5A mutant D1114N.
XX
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US021660.
XX
PR 09-AUG-1999; 99US-0147488P.
PR 17-MAR-2000; 2000US-0190057P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Splawski I;
XX
DR WPI; 2001-290564/30.
XX
PT New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT useful in diagostic/prognostic or drug screening methods, particularly in
PT mutational analyses for screening individuals with or at risk for long QT
PT syndrome.
XX

PS Claim 31; Page; 76pp; English.
XX
CC The present sequence is that of the claimed D1114N mutant of the human
CC SCN5A protein. The mutant is encoded by an SCN5A mutant gene in which a
CC G/A mutation alters codon 1114 from GAC to AAC. Mutations of the SCN5A
CC gene are implicated in Romano-Ward syndrome, the autosomal dominant form
CC of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene
CC lead to the following amino acid alterations in the encoded protein:
CC D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the
CC mutations provides means for assessing a risk in a human subject for
CC LQTS, for diagnosing a mutation which causes LQTS, and for screening for
CC drugs useful in treating a human having a mutation in the SCN5A gene.
CC Note: The present sequence is not shown in the specification but is
CC derived from the KVLQT-1 sequence given in the Sequence Listing (see
CC AAB82220)
XX
SQ Sequence 2016 AA;

Query Match 99.4%; Score 10427.5; DB 4; Length 2016;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2005; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||| |||| 
Db       1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
              |||| |  |||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db       1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQANWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860
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Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
```

RESULT 18
AAB82243
ID AAB82243 standard; protein; 2016 AA.
XX
AC AAB82243;
XX
DT 21-JUN-2001 (first entry)
XX
DE Human SCN5A mutant R1623L.
XX
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US021660.
XX
PR 09-AUG-1999; 99US-0147488P.
PR 17-MAR-2000; 2000US-0190057P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Splawski I;
XX
DR WPI; 2001-290564/30.
XX
PT New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT useful in diagostic/prognostic or drug screening methods, particularly in
PT mutational analyses for screening individuals with or at risk for long QT
PT syndrome.
XX
PS Claim 31; Page; 76pp; English.
XX
CC The present sequence is that of the claimed R1623T mutant of the human
CC SCN5A protein. The mutant is encoded by an SCN5A mutant gene in which a
CC G/T mutation alters codon 1623 from CGA to CTA. Mutations of the SCN5A
CC gene are implicated in Romano-Ward syndrome, the autosomal dominant form
CC of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene
CC lead to the following amino acid alterations in the encoded protein:
CC D1114N, L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the
CC mutations provides means for assessing a risk in a human subject for
CC LQTS, for diagnosing a mutation which causes LQTS, and for screening for
CC drugs useful in treating a human having a mutation in the SCN5A gene.
CC Note: The present sequence is not shown in the specification but is
CC derived from the KVLQT-1 sequence given in the Sequence Listing (see
CC AAB82220)
XX
SQ Sequence 2016 AA;

Query Match 99.4%; Score 10425.5; DB 4; Length 2016;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2005; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||  |||||  |||||||||||||||||||||||||||||||||||||||||
Db        541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy        961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy       1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db       1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy       1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
              |||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140
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Qy       1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy       1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy       1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy       1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy       1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy       1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy       1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy       1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy       1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 LFLVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy       1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy       1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
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RESULT 19
AAW23994
ID AAW23994 standard; protein; 2016 AA.
XX
AC AAW23994;
XX
DT 06-JUL-1998 (first entry)
XX
DE Human hH1 sodium channel protein.
XX
KW Ion channel; sodium channel; hH1; human; cardiac cell; heart; pacemaker;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO9802040-A1.
XX
PD 22-JAN-1998.
XX
PF 04-APR-1997; 97WO-US005556.
XX
PR 17-JUL-1996; 96US-00682433.
XX
PA (MEDT) MEDTRONIC INC.
XX
PI Stokes KB, Morissette J;
XX
DR WPI; 1998-110247/10.
DR N-PSDB; AAV09029.
XX
PT System for delivering genetic material to heart - comprises reservoir,
PT catheter and optionally pacing electrode for delivering ion-channel
PT protein, useful for, e.g. improving sensing by pacemaker.
XX
PS Disclosure; Page 41-47; 73pp; English.
XX
CC This protein comprises the human hH1 voltage-regulated sodium channel
CC protein that can be used in a novel system for enhancing cardiac dignal
CC sensing by cardiac pacemakers through genetic treatment. A claimed system
CC for delivering genetic material (GM) comprises a reservoir containing GM
CC and a device for delivering it to myocardial cells (MC) at a specific
CC location. The GM increases the amplitude of the cardiac signal, improving
CC the signal-to-noise (S/N) ratio that is sensed by the electrode of a
CC pacemaker. Also claimed are: (1) an implantable delivery system
CC comprising a reservoir for GM which increases the expression of ion
CC channels in MC and system for delivering this through a catheter, the tip
CC of which engages MC at the chosen location, and (2) a system similar to
CC (1) comprising a pacing electrode on an inner wall of the heart, close to
CC the site where the GM is delivered. The system is used for delivery of an
CC ion-channel GM which causes depolarisation of atrial and ventricular MC
CC and improves the sensing of cardiac signals by the pacemaker and the S/N
CC ratio of atrial P-waves. The preferred GM comprises DNA (see AAV09029) or
CC RNA encoding hH1
XX
SQ Sequence 2016 AA;

Query Match 99.4%; Score 10421.5; DB 2; Length 2016;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2004; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
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Qy       361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
Db       361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy       421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Db       421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy       481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Db       481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy       541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Db       541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy       601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Db       601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy       661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Db       661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy       721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Db       721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy       781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Db       781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db       841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db       901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy       961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db       961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy      1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
Db      1021 PTRKETQFEEGEQPGQGTPGDPDAVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy      1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
Db      1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy      1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
Db      1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy      1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
Db      1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy      1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
Db      1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy      1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
Db      1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy      1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
Db      1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy      1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
Db      1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy      1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
Db      1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy      1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
Db      1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1620

Qy      1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
Db      1621 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1680

Qy      1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
Db      1681 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1740

Qy      1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
Db      1741 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1800

Qy      1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
Db      1801 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1860

Qy      1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
Db      1861 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1920

Qy      1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
Db      1921 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1980

Qy      1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db      1981 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2016
```

RESULT 20
AAB82242
ID AAB82242 standard; protein; 2015 AA.
XX
AC AAB82242;
XX
DT 21-JUN-2001 (first entry)
XX
DE Human SCN5A mutant delF1617.
XX
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US021660.
XX
PR 09-AUG-1999; 99US-0147488P.
PR 17-MAR-2000; 2000US-0190057P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Splawski I;
XX
DR WPI; 2001-290564/30.
XX
PT New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT useful in diagostic/prognostic or drug screening methods, particularly in

PT mutational analyses for screening individuals with or at risk for long QT
PT syndrome.
XX
PS Claim 31; Page; 76pp; English.
XX
CC The present sequence is that of the claimed delF1617 mutant of the human
CC SCN5A protein. The mutant is encoded by an SCN5A mutant gene carrying a
CC deletion of the TTC codon for Phe-1617. Mutations of the SCN5A gene are
CC implicated in Romano-Ward syndrome, the autosomal dominant form of Long
CC QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene lead to
CC the following amino acid alterations in the encoded protein: D1114N,
CC L1501V, delF1617, R1623L, E1784K and S1787N. Knowledge of the mutations
CC provides means for assessing a risk in a human subject for LQTS, for
CC diagnosing a mutation which causes LQTS, and for screening for drugs
CC useful in treating a human having a mutation in the SCN5A gene. Note: The
CC present sequence is not shown in the specification but is derived from
CC the KVLQT-1 sequence given in the Sequence Listing (see AAB82220)
XX
SQ Sequence 2015 AA;

Query Match 99.3%; Score 10416; DB 4; Length 2015;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2005; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

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Qy     1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
Db     1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60

Qy    61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
Db    61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 120

Qy   121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
Db   121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 180

Qy   181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
Db   181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240

Qy   241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
Db   241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300

Qy   301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
Db   301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360

Qy   361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
Db   361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420

Qy   421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
Db   421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480

Qy   481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
Db   481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540

Qy   541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
Db   541 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600

Qy   601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
Db   601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660

Qy   661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
Db   661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720

Qy   721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
Db   721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780

Qy   781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
Db   781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840

Qy   841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900
Db   841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWI 900

Qy   901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960
Db   901 ETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQ 960

Qy   961 LALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020
Db   961 LALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETEKVP 1020

Qy  1021 PTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-QESQ 1079
Db  1021 PTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQESQ 1080

Qy  1080 PVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1139
Db  1081 PVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSEGS 1140

Qy  1140 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1199
Db  1141 TADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTCYH 1200

Qy  1200 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1259
Db  1201 IVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKWVA 1260

Qy  1260 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1319
Db  1261 YGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFEGM 1320

Qy  1320 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1379
Db  1321 RVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIVNN 1380

Qy  1380 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1439
Db  1381 KSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQPQW 1440

Qy  1440 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1499
Db  1441 EYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK 1500

Qy  1500 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1559
Db  1501 LGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKINIL 1560

Qy  1560 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFSPT 1619
Db  1561 AKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKY-FSPT 1619

Qy  1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679
Db  1620 LFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMANFA 1679

Qy  1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739
Db  1680 YVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGSRG 1739

Qy  1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799
Db  1740 DCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIWEK 1799

Qy  1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859
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Db       1800 FDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFTKR 1859

Qy       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1860 VLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRS 1919

Qy       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1920 LKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSYDSV 1979

Qy       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||||||||||||||||||||||||||||||
Db       1980 TRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015


RESULT 21
AAR67913
ID   AAR67913 standard; protein; 2019 AA.
XX
AC   AAR67913;
XX
DT   25-MAR-2003  (revised)
DT   05-AUG-1995  (first entry)
XX
DE   Cardiac sodium channel protein.
XX
KW   Sodium channel protein; therapeutic; diagnostic; prognostic;
KW   antiarrythmic; cardiant; cardioglycoside.
XX
OS   Rattus rattus.
XX
PN   US5380836-A.
XX
PD   10-JAN-1995.
XX
PF   30-SEP-1991;   91US-00768107.
XX
PR   13-FEB-1989;   89US-00331330.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Rogart RB;
XX
DR   WPI; 1995-060381/08.
DR   P-PSDB; AAQ81328.
XX
PT   Purified DNA's encoding rat and human cardiac sodium channel protein -
PT   useful for recombinant expression to produce sodium channel proteins.
XX
PS   Disclosure; Fig 2; 39pp; English.
XX
CC   The rat cardiac channel protein has various therapeutic, diagnostic and
CC   prognostic uses. It may also be used to develop more effective
CC   antiarrythmic, cardiant and cardioglycoside drugs. In Figure 2, the
CC   sequence is compared to the deduced amino acid sequence of rat brain II
CC   cDNA. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 2019 AA;

  Query Match             93.1%;  Score 9767;  DB 2;  Length 2019;
  Best Local Similarity   93.3%;  Pred. No. 0;
  Matches 1884;  Conservative   47;  Mismatches   84;  Indels    4;  Gaps    3;

Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQAR-GSTTLQESREGLPEEEAPRPQLDLQ 59
              ||| |||||||||||||||||||||||||||||| || | ||||||| |||||||||||
Db          1 MANLLLPRGTSSFRRFTRESLAAIEKRMAEKQARGGSATSQESREGLQEEEAPRPQLDLQ 60

Qy         60 ASKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHP 119
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASKKLPDLYGNPPRELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHP 120

Qy        120 IRRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILAR 179
              :|||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||

Db        121 VRRAAVKILVHSLFSMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILAR 180

Qy        180 GFCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTI 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GFCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTI 240

Qy        240 VGALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 VGALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTELNGTNGSVEADGL 300

Qy        300 VWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFA 359
              || |||:||:|| ||||||||:||||||||||||||||||||||||||||||||||||||
Db        301 VWNSLDVYLNDPANYLLKNGTTDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFA 360

Qy        360 WAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQ 419
              ||||||||||||||||:     :  ::      ||||||||||||||||||||||||||||
Db        361 WAFLALFRLMTQDCWERLFAWAFLALFRLMTQDCWLVIFLGSFYLVNLILAVVAMAYEEQ 420

Qy        420 NQATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRR 479
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :|||:||||
Db        421 NQATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVTNHERKSKRR 480

Qy        480 KRMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGS 539
              ||:|||||: |:|||||||||||||:| |||| |||||||:|||||||||||||||| ||
Db        481 KRLSSGTEDGGDDRLPKSDSEDGPRALNQLSLTHGLSRTSMRPRSSRGSIFTFRRRDQGS 540

Qy        540 EADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNG 599
              |||||||||||||||||||||||||||||| |||||| || ||||: |:||:||||||||
Db        541 EADFADDENSTAGESESHRTSLLVPWPLRHPSAQGQPGPGASAPGYVLNGKRNSTVDCNG 600

Qy        600 VVSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGAR 659
              ||||||||| |||||||:||||::|: |||||||||||||||||| |||| ||||||||||
Db        601 VVSLLGAGDAEATSPGSYLLRPMVLDRPPDTTTPSEEPGGPQMLTPQAPCADGFEEPGAR 660

Qy        660 QRALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFT 719
              |||||||||||||||||||| |||||||| || |||||||||||||||| || ||||||
Db        661 QRALSAVSVLTSALEELEESHRKCPPCWNRFAQHYLIWECCPLWMSIKQKVKFVVMDPFA 720

Qy        720 DLTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQ 779
              |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        721 DLTITMCIVLNTLFMALEHYNMTAEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQ 780

Qy        780 GWNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGAL 839
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        781 GWNIFDSIIVILSLMELGLSRMGNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGAL 840

Qy        840 GNLTLVLAIIVFIFAVVGMQLFGKNYSELRD--SDSGLLPRWHMMDFFHAFLIIFRILCG 897
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db        841 GNLTLVLAIIVFIFAVVGMQLFGKNYSELRHRISDSGLLPRWHMMDFFHAFLIIFRILCG 900

Qy        898 EWIETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMN 957
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 EWIETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDGEMN 960

Qy        958 NLQLALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETE 1017
              ||||||||||||||||||||||||:||:||:||||||  ||||||  | |||||| |
Db        961 NLQLALARIQRGLRFVKRTTWDFCCGILRRRPKKPAALATHSQLPSCITAPRSPPPPEVE 1020

Qy       1018 KVPPTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQE 1077
              |||| |||||||| ::|||||||| ||||||||||||:|||||||||||||||||||||||
Db       1021 KVPPARKETRFEEDKRPGQGTPGDSEPVCVPIAVAESDTEDQEEDEENSLGTEEESSKQE 1080

Qy       1078 SQPVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSE 1137
              || |||| |   : | ||||| | |||| || |||||:|: | ||||||||||||||| ||
Db       1081 SQVVSGGHEPYQEPRAWSQVSETTSSEAGASTSQADWQQEQKTEPQAPGCGETPEDSYSE 1140

Qy       1138 GSTADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTC 1197
              |||||||||:|||||||||:|||||||||||||||||||| |||||:||||||||||||
Db       1141 GSTADMTNTADLLEQIPDLGEDVKDPEDCFTEGCVRRCPCCMVDTTQSPGKVWWRLRKTC 1200

Qy       1198 YHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKW 1257
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 YRIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKW 1260
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Qy       1258 VAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFE 1317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 VAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFE 1320

Qy       1318 GMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIV 1377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIV 1380

Qy       1378 NNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQP 1437
             ||||:||| |:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 NNKSECESFNVTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQP 1440

Qy       1438 QWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAM 1497
             ||| |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 QWEDNLYMYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAM 1500

Qy       1498 KKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKIN 1557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db       1501 KKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKVN 1560

Qy       1558 ILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFS 1617
             ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ILAKINLLFVAIFTGECIVKMAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFS 1620

Qy       1618 PTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMAN 1677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 PTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMAN 1680

Qy       1678 FAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGS 1737
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       1681 FAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPNLPNSNGS 1740

Qy       1738 RGDCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIW 1797
             ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 RGNCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIW 1800

Qy       1798 EKFDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFT 1857
             |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 EKFDPEATQFIEYLALSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFT 1860

Qy       1858 KRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQ 1917
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1861 KRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSATVIQRAFRRHLLQ 1920

Qy       1918 RSLKHASFLFRQQA-GSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSSISSTSFPPSY 1976
             ||:||||||||||| |||||:|||||||||||:|: ||||   | ||||||||||||||||
Db       1921 RSVKHASFLFRQQAGGSGLSDEDAPEREGLIAYMMNGNFSRRSAPLSSSSISSTSFPPSY 1980

Qy       1977 DSVTRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
             |||||||||| || |||| ||||||||||||||||||||
Db       1981 DSVTRATSDNLPVRASDYSRSEDLADFPPSPDRDRESIV 2019
```

```
RESULT 22
AAR06584
ID   AAR06584 standard; protein; 2020 AA.
XX
AC   AAR06584;
XX
DT   10-JAN-1991  (first entry)
XX
DE   Cardiac sodium channel.
XX
KW   Rat; arrhythmia.
XX
OS   Rattus rattus.
XX
PN   WO9009391-A.
XX
PD   23-AUG-1990.
XX
PF   13-FEB-1989;   89US-00310330.
XX
PR   13-FEB-1989;   89US-00310330.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Rogart RB;
XX
DR   WPI; 1990-275095/36.
DR   N-PSDB; AAQ05831.
XX
PT   New rate cardiac sodium channel proteins - and associated DNA sequences,
PT   polypeptide(s) and peptide(s) associated with proteins, useful as
PT   antiarrhythmic and cardiotonic drugs.
XX
PS   Disclosure; Fig 2; 65pp; English.
XX
CC   The sequence deduced from cDNA derived from 3 overlapping clones, pRH3-
CC   1,pRH4-23, and pRH14-31. (Deposited as ATCC 67885, 67886, and 67887
CC   resp.) The clones were isolated from a cDNA library in the lambda Zap
CC   vector prepd. from mRNA obtd. from newborn rat hearts using rat brain II
CC   cDNA probe. The protein has diagnostic, therapeutic, and prognostic
CC   applications
XX
SQ   Sequence 2020 AA;
```

Query Match 92.7%; Score 9719; DB 2; Length 2020;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 1879; Conservative 44; Mismatches 92; Indels 4; Gaps 3;

```
Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQAR-GSTTLQESREGLPEEEAPRPQLDLQ 59
              ||| |||||||||||||||||||||||||||| || | ||||||| ||||||||||||
Db          1 MANLLLPRGTSSFRRFTRESLAAIEKRMAEKQARGGSATSQESREGLQEEEAPRPQLDLQ 60

Qy         60 ASKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHP 119
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASKKLPDLYGNPPPELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHP 120

Qy        120 IRRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILAR 179
              :|||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRRAAVKILVHSLFSMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILAR 180

Qy        180 GFCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTI 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GFCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTI 240

Qy        240 VGALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 VGALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTELNGTNGSVEADGL 300

Qy        300 VWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFA 359
              || |||:||:|| ||||||||:||||||||||||||||||||||||||||||||||||||
Db        301 VWNSLDVYLNDPANYLLKNGTTDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFA 360

Qy        360 WAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQ 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQ 420

Qy        420 NQATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRR 479
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :|||:||||
Db        421 NQATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVTNHERKSKRR 480

Qy        480 KRMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGS 539
              ||:|||||: |:|||||||||||||:| |||| |||||||:|||||||||||||| ||
Db        481 KRLSSGTEDGGDDRLPKSDSEDGPRALNQLSLTHGLSRTSMRPRSSRGSIFTFRRRDQGS 540

Qy        540 EADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNG 599
              ||         : : |||||||||||||  |||||| || |||||: |:||:|||||||||
Db        541 EALVPWPLRHPSAQGESHRTSLLVPWPLRHPSAQGQPGPGASAPGYVLNGKRNSTVDCNG 600

Qy        600 VVSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGAR 659
              |||||||||| |||||||:||||::|: |||||||||||||||||| |||| |||||||||
Db        601 VVSLLGAGDAEATSPGSYLLRPMVLDRPPDTTTPSEEPGGPQMLTPQAPCADGFEEPGAR 660
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Qy       660 QRALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFT 719
Db       661 QRALSAVSVLTSALEELEESHRKCPPCWNRFAQHYLIWECCPLWMSIKQKVKFVVMDPFA 720

Qy       720 DLTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQ 779
Db       721 DLTITMCIVLNTLFMALEHYNMTAEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQ 780

Qy       780 GWNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGAL 839
Db       781 GWNIFDSIIVILSLMELGLSRMGNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGAL 840

Qy       840 GNLTLVLAIIVFIFAVVGMQLFGKNYSELRD--SDSGLLPRWHMMDFFHAFLIIFRILCG 897
Db       841 GNLTLVLAIIVFIFAVVGMQLFGKNYSELRHRISDSGLLPRWHMMDFFHAFLIIFRILCG 900

Qy       898 EWIETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMN 957
Db       901 EWIETMWDCMEVSGQSLCLLVFLLVMVIGMEVSGQLFLALLLSSFSADNLTAPDEDGEMN 960

Qy       958 NLQLALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETE 1017
Db       961 NLQLALARIQRGLRFVKRTTWDFCCGILRRRPKKPAALATHSQLPSCITAPRSPPPPEVE 1020

Qy      1018 KVPPTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQE 1077
Db      1021 KVPPARKETRFEEDKRPGQGTPGDSEPVCVPIAVAESDTEDQEEDEENSLGTEEESSKQE 1080

Qy      1078 SQPVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCSE 1137
Db      1081 SQVVSGGHEPYQEPRAWSQVSETTSSEAGASTSQADWQQEQKTEPQAPGCGETPEDSYSE 1140

Qy      1138 GSTADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKTC 1197
Db      1141 GSTADMTNTADLLEQIPDLGEDVKDPEDCFTEGCVRRCPCCMVDTTQSPGKVWWRLRKTC 1200

Qy      1198 YHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKW 1257
Db      1201 YRIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLKW 1260

Qy      1258 VAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFE 1317
Db      1261 VAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRFE 1320

Qy      1318 GMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIV 1377
Db      1321 GMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPLNYTIV 1380

Qy      1378 NNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQP 1437
Db      1381 NNKSECESFNVTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEEQP 1440

Qy      1438 QWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAM 1497
Db      1441 QWEDNLYMYIYFVVFIIFGSFFTLNLFIGVIIVVFNQQKKKLGGQDIFMTEEQKKYYNAM 1500

Qy      1498 KKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKIN 1557
Db      1501 KKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDDQSPEKVN 1560

Qy      1558 ILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYFFS 1617
Db      1561 ILAKINLLFVAIFTGECIVKMAALRHYYFTNSWNIFDFVVVILSIVGTVLSDIIQKYLLS 1620

Qy      1618 PTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMAN 1677
Db      1621 PTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMAN 1680

Qy      1678 FAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPTLPNSNGS 1737
Db      1681 FAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTGPPYCDPNLPNSNGS 1740

Qy      1738 RGDCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIW 1797
Db      1741 RGNCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEESTEPLSEDDFDMFYEIW 1800

Qy      1798 EKFDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFT 1857
Db      1801 EKFDPEATQFIEYLALSDFADALSEPLRIAKPNQISLINMDLPMVSGDRIHCMDILFAFT 1860

Qy      1858 KRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSAMVIQRAFRRHLLQ 1917
Db      1861 KRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEVSATVIQRAFRRHLLQ 1920

Qy      1918 RSLKHASFLFRQQA-GSGLSEEDAPEREGLIAYVMSENFSRPLGPPSSSSISSTSFPPSY 1976
Db      1921 RSVKHASFLFRQQAGGSGLSDEDAPEREGLIAYMMNGNFSRRSAPLSSSSISSTSFPPSY 1980

Qy      1977 DSVTRATSDNLQVRGSDYSHSEDLADFPPSPDRDRESIV 2015
Db      1981 DSVTRATSDNLPVRASDYSRSEDLADFPPSPDRDRESIV 2019
```

RESULT 23
AAU19518
ID AAU19518 standard; protein; 1603 AA.
XX
AC AAU19518;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human diagnostic and therapeutic polypeptide (DITHP) #104.
XX
KW Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;
KW cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;
KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;
KW respiratory disorder.
XX
OS Homo sapiens.
XX
PN WO200162927-A2.
XX
PD 30-AUG-2001.
XX
PF 21-FEB-2001; 2001WO-US006059.
XX
PR 24-FEB-2000; 2000US-0184693P.
PR 24-FEB-2000; 2000US-0184697P.
PR 24-FEB-2000; 2000US-0184698P.
PR 24-FEB-2000; 2000US-0184768P.
PR 24-FEB-2000; 2000US-0184769P.
PR 24-FEB-2000; 2000US-0184770P.
PR 24-FEB-2000; 2000US-0184771P.
PR 24-FEB-2000; 2000US-0184772P.
PR 24-FEB-2000; 2000US-0184773P.
PR 24-FEB-2000; 2000US-0184774P.
PR 24-FEB-2000; 2000US-0184776P.
PR 24-FEB-2000; 2000US-0184777P.
PR 24-FEB-2000; 2000US-0184797P.
PR 24-FEB-2000; 2000US-0184813P.
PR 24-FEB-2000; 2000US-0184837P.
PR 24-FEB-2000; 2000US-0184841P.
PR 24-FEB-2000; 2000US-0185213P.
PR 24-FEB-2000; 2000US-0185216P.
PR 12-MAY-2000; 2000US-0203785P.
PR 15-MAY-2000; 2000US-0204226P.
PR 16-MAY-2000; 2000US-0204525P.
PR 16-MAY-2000; 2000US-0204821P.
PR 16-MAY-2000; 2000US-0204908P.
PR 16-MAY-2000; 2000US-0205232P.
PR 17-MAY-2000; 2000US-0204815P.
PR 17-MAY-2000; 2000US-0204863P.
PR 17-MAY-2000; 2000US-0205221P.
PR 17-MAY-2000; 2000US-0205285P.
PR 17-MAY-2000; 2000US-0205286P.
PR 17-MAY-2000; 2000US-0205287P.

PR 17-MAY-2000; 2000US-0205323P.
PR 17-MAY-2000; 2000US-0205324P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
PI Chen A, D'sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour GE;
PI Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF;
PI Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A;
PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;
PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
XX
DR WPI; 2001-502867/55.
DR N-PSDB; AAS31089.
XX
PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.
PT enzymes, hormones and receptors, useful in diagnostics and therapeutics.
XX
PS Claim 27; Page 457-460; 522pp; English.
XX
CC The invention relates to polynucleotides (I) encoding diagnostic and
CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and
CC proteins involved in growth and development and receptors. (I) and (II)
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate DITHP expression. For example, (I) and (II)
CC may be used to treat disorders associated with decreased polypeptide
CC expression by rectifying mutations or deletions in a patient's genome,
CC that affect the activity of the DITHPs, by expressing inactive proteins
CC or supplementing the patient's own production of them. (I) and (II) may
CC be used to treat diseases, for example, cell proliferative disorder,
CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,
CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally,
CC (I) may be used to produce the DITHPs, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. (I) and
CC its complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids in
CC samples, and therefore which patients may be in need of restorative
CC therapy. (II) may also be used as antigens in the production of
CC antibodies against DITHPs and in assays to identify modulators of DITHP
CC expression and activity. The anti-DITHP antibodies and antagonists may
CC also be used to down regulate expression and activity. The anti-DITHP
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAU19415-AAU19625 represent human diagnostic and therapeutic
CC (DITHP) polypeptides of the invention
XX
SQ Sequence 1603 AA;

Query Match 73.0%; Score 7659.5; DB 4; Length 1603;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 1464; Conservative 31; Mismatches 47; Indels 5; Gaps 3;

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Qy          1 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 MANFLLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQA 110

Qy         61 SKKLPDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPI 120
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        111 SKKLPDLYQNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPV 170

Qy        121 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 RRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARA 230

Qy        181 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 FCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIV 290

Qy        241 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 GALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTALNGTNGSVEADGLV 350

Qy        301 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 WESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENPDHGYTSFDSFAW 410

Qy        361 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 AFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLILAVVAMAYEEQN 470

Qy        421 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 QATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSRSSLEMSPLAPVNSHERRSKRRK 530

Qy        481 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 RMSSGTEECGEDRLPKSDSEDGPRAMNHLSLTRGLSRTSMKPRSSRGSIFTFRRRDLGSE 590

Qy        541 ADFADDENSTAGESESHRTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 600
              |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db        591 ADFADDENSTARESESHHTSLLVPWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGV 650

Qy        601 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 VSLLGAGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQ 710

Qy        661 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 RALSAVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTD 770

Qy        721 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 LTITMCIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQG 830

Qy        781 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 WNIFDSIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALG 890

Qy        841 NLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGL---LPRWHMMDFFHAFLIIFRILCG 897
              |||||||||||||:|| || |:||   | : |      ||||| |||||:|||:||||||
Db        891 NLTLVLAIIVFIFALVGKQLLGENYRNNRKNISAPHEDWPRWHMHDFFHSFLIVFRILCG 950

Qy        898 EWIETMWDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMN 957
              |||| || |||| :|:||::|| |||:|||||||||:||||:||||||||::| |:|
Db        951 EWIENMWACMEVGQKSICLILFLTVMVLGNLVVLNLFIALLLNSFSADNLTAPEDDGEVN 1010

Qy        958 NLQLALARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETE 1017
              |||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1011 NLQVALARIQRGLRFVKRTTWDFCCGLLRHRPQKPAALAAQGQLPSCIATPYSPPPPETE 1070

Qy       1018 KVPPTRKETRFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSK-Q 1076
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1071 KVPPTRKETQFEEGEQPGQGTPGDPEPVCVPIAVAESDTDDQEEDEENSLGTEEESSKQQ 1130

Qy       1077 ESQPVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCS 1136
              ||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 ESQPVSGWPRGPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAPGCGETPEDSCS 1190

Qy       1137 EGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKT 1196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 EGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTTQAPGKVWWRLRKT 1250

Qy       1197 CYHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLK 1256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 CYHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADKMFTYVFVLEMLLK 1310

Qy       1257 WVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRF 1316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 WVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRALSRF 1370

Qy       1317 EGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPL-NYT 1375
              |||||||||||||||||||||||||||||||||||||||||||||||||| |:|:  |  :
Db       1371 EGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINYTDGEFSLVPLS 1430

Qy       1376 IVNNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRGYEE 1435
              |||||| |:  | ||  :|  ||||||||  |||||||||||||||||||||||||||
```

```
Db       1431 IVNNKSDCKIQNSTGSFFWVNVKVNFDNVAMGYLALLQVATFKGWMDIMYAAVDSREVNM 1490

Qy       1436 QPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYN 1495
              ||:|| |:|||:|||||||| |||||||:|||||||||||||||||||||||||||||||
Db       1491 QPKWEDNVYMYLYFVIFIIFGGFFTLNLFVGVIIDNFNQQKKKLGGQDIFMTEEQKKYYN 1550

Qy       1496 AMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMV 1542
              |||||||||||||||||:|||:|||||:||||:||| |||||||
Db       1551 AMKKLGSKKPQKPIPRPLNKFQGFVFDIVTRQAFDITIMVLICLNMV 1597


RESULT 24
ADP79541
ID   ADP79541 standard; protein; 2000 AA.
XX
AC   ADP79541;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human sodium III channel splice variant (hNAIII18).
XX
KW   Human; sodium III channel; hNAIII18; splice variant; antiarrhythmic;
KW   analgesic.
XX
OS   Homo sapiens.
XX
PN   WO2004050857-A2.
XX
PD   17-JUN-2004.
XX
PF   04-DEC-2003; 2003WO-US038796.
XX
PR   04-DEC-2002; 2002US-0431794P.
XX
PA   (EURO-) EUROCELTIQUE SA.
XX
PI   Kammesheidt A,  Hodges D;
XX
DR   WPI; 2004-450725/42.
DR   N-PSDB; ADP79540.
XX
PT   New human sodium III channel, useful in treating cardiac arrhythmias,
PT   herpes virus infection, diabetes mellitus, or vasculitis.
XX
PS   Claim 9; SEQ ID NO 2; 101pp; English.
XX
CC   The present sequence is that of a novel splice variant of the human
CC   sodium III channel alpha subunit, denoted hNAIII18. The cDNA was cloned
CC   by RT-PCR from human embryonic brain total RNA using human NaIII specific
CC   primers ADP79546-ADP79547. The hNaIII18 sequence contains an additional
CC   49 amino acid residues that do not appear in a previously reported human
CC   NaIII ADP79543, and also differs from a previously reported splice
CC   variant of human sodium channel alpha subunit ADP79545 by 12 amino acids
CC   out of 2000. Transient transfection of HEK293 cells by hNaIII18 resulted
CC   in expression of functional sodium channels. The invention provides:
CC   hNaIII18 proteins and their fragments and derivatives; hNaIII18-encoding
CC   nucleic acids and their fragments, including primers, probes, and
CC   regulatory sequences; hNaIII18-specific antibodies; and methods of using
CC   these materials to detect the presence of hNaIII18 proteins or nucleic
CC   acids. The invention also provides an assay method for screening to
CC   identify selective modulators of hNaIII18 expression or activity. These
CC   may be useful for treatment of conditions associated with sodium channel
CC   over- or under-expression, e.g. for treatment of cardiac arrhythmia,
CC   neuronal disorders, nociceptive pain-related diseases and neuropathic
CC   pain-related diseases, e.g. pain from peripheral nerve trauma, herpes
CC   virus infection, diabetes mellitus, causalgia, plexus avulsion, neuroma,
CC   limb amputation or vasculitis.
XX
SQ   Sequence 2000 AA;

  Query Match             61.1%;  Score 6406.5;  DB 8;  Length 2000;
  Best Local Similarity   62.8%;  Pred. No. 0;
  Matches 1297;  Conservative  232;  Mismatches  366;  Indels  171;  Gaps   28;

Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||||| ||::|:     |::     :|  |:|  ||:| | |
Db          6 LVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDN----DDENKPKPNSDLEAGKNL 61

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              | :||: | |:: ||||||||:|  :|||||:|||| |||||||:|||:|:| :|:|: |
Db         62 PFIYGDIPPEMVSEPLEDLDPYYINKKTFIVMNKGKAIFRFSATSALYILTPLNPVRKIA 121

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||:|||||||||||||   :|| ||| |||||| |||||||:|||||||||
Db        122 IKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 181

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||||:||| |||| |||||||||||||||||||||| ||||||||||
Db        182 DFTFLRDPWNWLDFSVIVMAYVTEFVSLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 241

Qy        245a QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTAL------- 287
              ||||||:|||:||||||||||||||||||:||::        | |:
Db        242 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFNGTMDS 301

Qy        288 NGTNGSVEADGLVWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGEN 347
              |||  :|      |:    |: |  :: : :|  | ||||| |||| ||||| |:||| |
Db        302 NGTFVNVTMSTFNWKD---YIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGYICVKAGRN 358

Qy        348 PDHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNL 407
              |::|||||:|:||||:|||||||| || ||| |||:||| |||||:|||||||||||||
Db        359 PNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLVNL 418

Qy        408 ILAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALT--------------IRGV 453
              |||||||||||||||: | |:||  ||: :| |||: |                | |:
Db        419 ILAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGIGGL 478

Qy        454 DTVSRSSLEMSPLAPVNSHERRSKRRKRMS----SGTEECGEDRLPKSDSEDGPRAMNHL 509
                :  || | | |:  :: | |::|:||       |  :   |  |||:||| :  : |
Db        479 GELLESSSEASKLSSKSAKEWRNRRKKRRRREHLEGNNKGERDSFPKSESEDSVKRSSFL 538

Qy        510 SLTRGLSRTSMKP------------------RSSRGSIFTFRRR--DLGSEADFADDEN 548
                  |  || |                    |:|: |||:|| |  |:||| ||||||:
Db        539 FSMDGNRLTSDKKFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEH 598

Qy        549 STAGESESHRTSLLVP--WPLRRTSAQGQPSPGT-SAPGHALHGKKNSTVDCNGVVSLLG 605
              ||  :||| | || ||     || |   | |  :   ||   :|| :|||||||||||:|
Db        599 STFEDSESRRDSLFVPHRHGERRNSNVSQASMSSRMVPGLPANGKMHSTVDCNGVVSLVG 658

Qy        606 AGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSA 665
              |   |||  |        ||: || :|    : |:|   ::  |:   ||||:|
Db        659 -GPSALTSPTGQL--------PPEGTT-TETEVRKRRLSSYQISMEMLEDSSGRQRAVSI 708

Qy        666 VSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITM 725
              |:||: :||||||| |||||| | |  :|||:||  |: :|  | |:|||| || ||:
Db        709 ASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDPFVDLAITI 768

Qy        726 CIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFD 785
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db        769a CIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPYYYFQEGWNIFD 828

Qy        786 SIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLV 845
              |||  |||||||| :  |||||||||||||||||||||||| |||||||||||||||||
Db        829 GIIVSLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLV 888

Qy        846 LAIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETM 903
              |||||||||||||||:|  |   : :|   |||||| ||||:|||:||:|||||||||
Db        889 LAIIVFIFAVVGMQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETM 948

Qy        904 WDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLAL 963
              ||||||:||::||:||:|||||||||||||||||||||:||| | |:| ||||||:|:
Db        949 WDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAV 1008

Qy        964 ARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVPPTR 1023
              |:|:|: :||    : |       | |   :   :: ||::           ::
Db       1009 GRMQKGIDYVKNKMRE-CFQKAFFRKPKVIEIHEGNKIDSCMSNNTG------IEISKEL 1061
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```
Qy       1024 KETRFEEGEQPGQGTPGDPE------------------PVCVPIAVAESDTDDQEEDEEN 1065
Db       1062 NYLRDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFE-------- 1113

Qy       1066 SLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAP 1125
Db       1114 NLNTEEFSSESELE------------ESKEKLNATSS----------------------- 1138

Qy       1126 GCGETPEDSCSEGSTAD--MTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTT 1183
Db       1139 ----------SEGSTVDVVLPREGEQAETEPE--EDLK-PEACFTEGCIKKFPFCQVSTE 1185

Qy       1184 QAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADK 1243
Db       1186 EGKGKIWWNLRKTCYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADK 1245

Qy       1244 MFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRT 1303
Db       1246 VFTYIFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRT 1305

Qy       1304 LRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCI 1363
Db       1306 LRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCV 1365

Qy       1364 NQTEGDLPLNYTIVNNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDI 1423
Db       1366 NMTTGNM-FDISDVNNLSDCQALG--KQARWKNVKVNFDNVGAGYLALLQVATFKGWMDI 1422

Qy       1424 MYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQD 1483
Db       1423 MYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQD 1482

Qy       1484 IFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVT 1543
Db       1483 IFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVT 1542

Qy       1544 MMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIV 1603
Db       1543 MMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLRLVSLRHYYFTIGWNIFDFVVVILSIV 1602

Qy       1604 GTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLL 1663
Db       1603 GMFLAEMIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLL 1662

Qy       1664 FLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTG 1723
Db       1663 FLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSA 1722

Qy       1724 PPYCDP-TLPNSNGSRGDCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEEST 1782
Db       1723 PPDCDPDTIHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESA 1782

Qy       1783 EPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMV 1842
Db       1783 EPLSEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAALDPPLLIAKPNKVQLIAMDLPMV 1842

Qy       1843 SGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEV 1902
Db       1843 SGDRIHCLDILFAFTKRVLGESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQEEV 1902

Qy       1903 SAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPP 1962
Db       1903 SAAIIQRNFRCYLLKQRLKNISSNYNKEAIKG--RIDLPIKQDMIIDKLNGNST----PE 1956

Qy       1963 SSSSISSTSFPPSYDSVTRATSDNLQ 1988
Db       1957 KTDGSSSTTSPPSYDSVTKPDKEKFE 1982
```

RESULT 25
AAB99676
ID AAB99676 standard; protein; 2005 AA.
XX

AC AAB99676;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN2A protein sequence SEQ ID NO:35.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55793.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 123-130; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 61.0%; Score 6394.5; DB 4; Length 2005;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 1301; Conservative 231; Mismatches 360; Indels 201; Gaps 33;

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Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
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Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348

Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408

Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR---------------GV 453

Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAASAESRDFSGAGGI 480

Qy        454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504

Db        481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy        505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549

Db        540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy        550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606

Db        600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy        607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666

Db        659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy        667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726

Db        709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy        727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786

Db        769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy        787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846

Db        829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy        847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904

Db        889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964

Db        949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017

Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050

Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110

Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170

Db       1146 ---------VDIGAPAEGEQPE-----------VEPEESLE-----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230

Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290

Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294
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Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350

Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRAVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407

Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467

Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527

Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587

Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647

Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707

Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766

Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVVNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826

Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886

Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946

Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999

Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995
```

RESULT 26
ADY27148
ID ADY27148 standard; protein; 2005 AA.
XX
AC ADY27148;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human SCN2A variant R223Q.
XX
KW SCN2A; anticonvulsant; muscular-Gen.; neuroprotective; antiarrhythmic;
KW antimigraine; nootropic; antiparkinsonian; neuroleptic; tranquilizer;
KW antidepressant; analgesic; nephrotropic; antidiabetic; cytostatic;
KW diagnostic; anxiety disorder; major depressive disorder; epilepsy;
KW paralysis; hyperthermia; myasthenia gravis; heart arrhythmia; ataxia;
KW migraine; Alzheimers disease; Parkinsons disease; cystic fibrosis; pain;
KW inflammation; polycystic kidney disease; phobia; schizophrenia;
KW neuropathic pain; hyperglycemia; hyperinsulinemia; sodium channel;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX

```
FH   Key             Location/Qualifiers
FT   Misc-difference 892
FT                   /label= V892I
FT                   /note= "wild-type Val substituted with Ile"
XX
PN   WO2005014863-A1.
XX
PD   17-FEB-2005.
XX
PF   06-AUG-2004; 2004WO-AU001051.
XX
PR   07-AUG-2003; 2003AU-00904154.
XX
PA   (BION-) BIONOMICS LTD.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE,  Davy A;
XX
DR   WPI; 2005-195767/20.
DR   N-PSDB; ADY27076.
XX
PT   Identifying subject predisposed to disorder associated with ion channel
PT   dysfunction, involves determining presence of specific mutation event in
PT   genes encoding ion channel subunits.
XX
PS   Claim 20; SEQ ID NO 84; 347pp; English.
XX
CC   This invention describes a novel method of identifying a subject
CC   predisposed to disorder associated with ion channel dysfunction
CC   comprising ascertaining whether at least one of the genes encoding ion
CC   channel subunits in the subject has undergone a mutation. The invention
CC   also describes 1) isolated nucleic acid molecules encoding an isolated
CC   polypeptide which is a mutant or variant ion channel subunit (including a
CC   mutant KCNQ2 subunit, where the mutation event has occurred in C terminal
CC   domain of the subunit and leads to disturbance in the calmodulin binding
CC   affinity of the subunit) and 2) an expression vector, cells, antibodies
CC   and a method for producing a non-human transgenic animal which are all
CC   used for screening of candidate pharmaceutical agents for diagnosing or
CC   treating epilepsy or a disorder associated with ion channel dysfunction.
CC   The mutation detected in the method disrupts the functioning of an
CC   assembled ion channel so as to produce an epilepsy phenotype in the
CC   subject or produces one or more disorders associated with ion channel
CC   dysfunction such as hyper- or hypo-kalemic periodic paralysis, myotonias,
CC   malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,
CC   migraine, Alzheimer's disease, Parkinson's disease, schizophrenia,
CC   anxiety, depression, phobic obsessive symptoms, neuropathic pain,
CC   inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic
CC   kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy,
CC   cystic fibrosis, congenital stationary night blindness and total color-
CC   blindness in the subject or to produce an epilepsy phenotype when
CC   expressed in combination with one or more additional mutations or
CC   variations in the ion channel subunit genes. The products of the
CC   invention have anticonvulsant, muscular-Gen., neuroprotective,
CC   antiarrhythmic, antimigraine, nootropic, antiparkinsonian, neuroleptic,
CC   tranquilizer, antidepressant, analgesic, nephrotropic, antidiabetic and
CC   cytostatic activity. This sequence represents a fragment of the human
CC   sodium ion channel subunit SCN2A encoded by exon 16 which contains the
CC   mutation V892I.
XX
SQ   Sequence 2005 AA;
```

Query Match 61.0%; Score 6394.5; DB 9; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;
Matches 1300; Conservative 233; Mismatches 359; Indels 201; Gaps 33;

```
Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||||:|:||::|:     :: |:   :|  |:|  ||:| | |
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              | :||: | |::  |||||||:|  :||||||||| | ||||| |||:|:||:|||: |
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||||||||||||||||||    :|| ||| |||||| |||||||:|||||||||
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||:||  || |||||||||||||||||||||||||| ||||||||||
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
              ||||||:|||:|||||||||||||||||||:||::          | |:  | |:
Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
              : :|  :       : | |: |  ::    | :| |||||||||| ||||| |:||| ||
Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
              ::|||||:|:||||:|||||||| || ||| |||:||| |||||:||||||||:|||
Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR----------------GV 453
              |||||||||||||: | |:||  ||: :| |||: |                    |:
Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAASAESRDFSGAGGI 480

Qy        454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
              | ||   | |:  :  |   || |:::  || ||   ||: ||:|||  |
Db        481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy        505 -------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
                          :  | ||           |:|| |:|:|| |  |:||| ||||||:|
Db        540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy        550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
              |  :::| | || ||     || |   | | :   |   ::|| :| |||||||||:|
Db        600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy        607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
              |    || |  |         |  ||| :|     :  :|    :|  |:|  :||||:|
Db        659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy        667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
              |:||: :||||||| |||||| : |   |||:||  |: :|  | |||||| || ||:|
Db        709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy        727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db        769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy        787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
              || |||||||: :  |||||||||||||||||||||||||||||||||||||||||||||
Db        829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy        847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
              |||:|||||||||||||:| |   : |:   |||||| |||:|||:||:||||||||||
Db        889 AIIIFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
              |||||:||::|| ||::|||||||||||||||||||||:||| | |:| ||||||:|:
Db        949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
              |:|:|: ||||    :|   : :   :|  ||           :  |||:
Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
                  | | |:     : | ||                          :|   | ||||
Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
              | ||| :        :| ||| ||: : :             :  :::||:|||
Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
```

```
                    :  ||  || ||                | ||           || ||||
Db       1146 ---------VDIGAPAEGEQPE-----------VEPEESLE-----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
              |||:  || :   :  ||:|| |||||| ||||:|||||:|||||||||||||||||:|:
Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
              ||||| :||||||:|||:|:|||||||||||: |||||||||||||||||||||  || |
Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
              |::|:| |||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
              |||||||||  ||| | |::  : ::||| |:|::|   | |     |  |||||||| |
Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
              ||:||||||||||||||||||  | ||::| |||||:||||||||||||||||||||||
Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
              |||||||||| |||||||||||||||||||||||||||||| ||:|| :|| ||||
Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
                ||::|| |||||||||||||||  |  |||  |||:|: :|||||::|| :||:||||
Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
                |||||||||||||||  |:::|:||| |||||||||||||||||:||||||||||
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
              |||||||||||||||||||||:||||:|||||| | |||||||:|| |||:||||||
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
              |||||||||:||||:||| |||    :   | :||||:|:||| || :|||||||:|:|||
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
              ||:|||||||||||| |||||||:||||:||||||:|||||:: ||||||||   || |
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
              ||||:: || |||||||||||||:|||||||||||||||||||:|||||:|||:|||||:
Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
              |||||||||:|| |||||::||||:||:||:: :|  | ::::  |     :  | :|
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
              :   ::|| :    |  :    ||: |||||||:   :  :    | |  ||
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995
```

RESULT 27
ADY27149
ID ADY27149 standard; protein; 2005 AA.
XX
AC ADY27149;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human SCN2A variant R223Q.
XX
KW SCN2A; anticonvulsant; muscular-Gen.; neuroprotective; antiarrhythmic;
KW antimigraine; nootropic; antiparkinsonian; neuroleptic; tranquilizer;
KW antidepressant; analgesic; nephrotropic; antidiabetic; cytostatic;
KW diagnostic; anxiety disorder; major depressive disorder; epilepsy;
KW paralysis; hyperthermia; myasthenia gravis; heart arrhythmia; ataxia;
KW migraine; Alzheimers disease; Parkinsons disease; cystic fibrosis; pain;
KW inflammation; polycystic kidney disease; phobia; schizophrenia;
KW neuropathic pain; hyperglycemia; hyperinsulinemia; sodium channel;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1003
FT /label= L1003I
FT /note= "wild-type Leu substituted with Ile"
XX
PN WO2005014863-A1.
XX
PD 17-FEB-2005.
XX
PF 06-AUG-2004; 2004WO-AU001051.
XX
PR 07-AUG-2003; 2003AU-00904154.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE, Davy A;
XX
DR WPI; 2005-195767/20.
DR N-PSDB; ADY27077.
XX
PT Identifying subject predisposed to disorder associated with ion channel
PT dysfunction, involves determining presence of specific mutation event in
PT genes encoding ion channel subunits.
XX
PS Claim 20; SEQ ID NO 85; 347pp; English.
XX
CC This invention describes a novel method of identifying a subject
CC predisposed to disorder associated with ion channel dysfunction
CC comprising ascertaining whether at least one of the genes encoding ion
CC channel subunits in the subject has undergone a mutation. The invention
CC also describes 1) isolated nucleic acid molecules encoding an isolated
CC polypeptide which is a mutant or variant ion channel subunit (including a
CC mutant KCNQ2 subunit, where the mutation event has occurred in C terminal
CC domain of the subunit and leads to disturbance in the calmodulin binding
CC affinity of the subunit) and 2) an expression vector, cells, antibodies
CC and a method for producing a non-human transgenic animal which are all
CC used for screening of candidate pharmaceutical agents for diagnosing or
CC treating epilepsy or a disorder associated with ion channel dysfunction.
CC The mutation detected in the method disrupts the functioning of an
CC assembled ion channel so as to produce an epilepsy phenotype in the
CC subject or produces one or more disorders associated with ion channel
CC dysfunction such as hyper- or hypo-kalemic periodic paralysis, myotonias,
CC malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,
CC migraine, Alzheimer's disease, Parkinson's disease, schizophrenia,
CC anxiety, depression, phobic obsessive symptoms, neuropathic pain,
CC inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic
CC kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy,
CC cystic fibrosis, congenital stationary night blindness and total color-
CC blindness in the subject or to produce an epilepsy phenotype when
CC expressed in combination with one or more additional mutations or
CC variations in the ion channel subunit genes. The products of the
CC invention have anticonvulsant, muscular-Gen., neuroprotective,
CC antiarrhythmic, antimigraine, nootropic, antiparkinsonian, neuroleptic,
CC tranquilizer, antidepressant, analgesic, nephrotropic, antidiabetic and
CC cytostatic activity. This sequence represents a fragment of the human
CC sodium ion channel subunit SCN2A encoded by exon 17 which contains the
CC mutation L1003I.
XX
SQ Sequence 2005 AA;

Query Match 61.0%; Score 6393.5; DB 9; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;

```
  Matches 1300;  Conservative  233;  Mismatches  359;  Indels  201;  Gaps   33;

Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR----------------GV 453
Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAASAESRDFSGAGGI 480

Qy        454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
Db        481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy        505 -------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
Db        540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy        550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
Db        600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy        607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
Db        659 GPSTLTSAGQLL--------PEGTTTETEI--KRRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy        667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
Db        709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy        727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
Db        769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy        787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
Db        829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy        847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
Db        889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
Db        949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNIQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
Db       1146 ---------VDIGAPAEGEQPE-----------VEPEESLE----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995

RESULT 28
ABB83627
ID   ABB83627 standard; protein; 2005 AA.
```

```
XX
AC   ABB83627;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human GEFS+ protein with SCN2A mutation.
XX
KW   Human; GEFS+; SCN2A; mutant; mutein;
KW   generalized epilepsy with febrile seizure plus.
XX
OS   Homo sapiens.
XX
PN   JP2002136289-A.
XX
PD   14-MAY-2002.
XX
PF   01-NOV-2000; 2000JP-00334969.
XX
PR   01-NOV-2000; 2000JP-00334969.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (RIKA ) RIKAGAKU KENKYUSHO.
XX
DR   WPI; 2002-552308/59.
DR   N-PSDB; ABQ79201.
XX
PT   A human polynucleotide which is complementary to an mRNA transcribed from
PT   a generalized epilepsy with febrile seizure plus (GEFS+)-related gene
PT   useful for diagnosing GEFS+.
XX
PS   Claim 10; Page 29-34; 37pp; Japanese.
XX
CC   This invention relates to a human polynucleotide which is complementary
CC   to an mRNA transcribed from a "generalized epilepsy with febrile seizure
CC   plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFS+. The
CC   present sequence represents the human GEFS+ protein sequence with SCN2A
CC   mutation
XX
SQ   Sequence 2005 AA;

  Query Match             60.9%;  Score 6392.5;  DB 5;  Length 2005;
  Best Local Similarity   62.1%;  Pred. No. 0;
  Matches 1300;  Conservative  232;  Mismatches  360;  Indels  201;  Gaps   33;

Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| ||||||||||:|:||::|:     :: |:   :|  |:|  ||:| | |
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              | :||: | |::  |||||||:|  :|||||||||| | ||||| |||:|:||:|||: |
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||||||||||||||||    :|| ||| ||||||  |||||||:|||||||||
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||:||  || |||||||||||||||||||||||||| ||||||||||
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
              ||||||:|||:|||||||||||||||||||:||::          | |:    | |:
Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
              : :|  :       : | |: |  ::    | :| |||||||||| ||||| |:||| ||
Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
              ::|||||:|:||||:|||||||| || ||| |||:||| |||||:||||||||||:|||
Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR--------------GV 453
              ||||||||||||||: | |:||  ||: :| |||: |                   |:
Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAAASAESRDFSGAGGI 480

Qy        454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
                | ||   | |:  :  |   || |:::  || ||   ||: ||:||| |
Db        481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVRKSESEDSIRRKGFRF 539

Qy        505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
                         :  | ||          |:|| |:|:|| |  |:||| ||||||:|
Db        540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy        550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
              |  :::| | || ||     || |   | |  :   |   ::|| :| |||||||||:|
Db        600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy        607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
              |    || |  |         |  ||| :|     :  :|    :|  |:| :||||:|
Db        659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy        667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
              |:||: :||||||| |||||| : |   |||:||  |: :|  | ||||||| || ||:|
Db        709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy        727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db        769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy        787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
              || |||||||: :  |||||||||||||||||||| ||||||||||||||||||||||
Db        829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy        847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
              |||||||||||||||:| |   : |:   |||||| ||||:|||:||:||||||||||
Db        889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
              |||||:||::|| ||::|||||||||||||||||||:||| | |:| ||||||:|:
Db        949aDCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
              |:|:|: ||||   :|   : :   :|  ||          :  |||:
Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
                  | | |:      : | ||                      :|   | ||||
Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
              | ||| :        :| ||| ||: : :             :  :::||:|||
Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
                    :  ||  || ||                | ||           || ||||
Db       1146 ---------VDIGAPAEGEQPE-----------VEPEESLE-----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
              |||:  || :   :  ||:|| |||||  ||||:||||||:|||||||||||||||:|:
Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
              ||||| :||||||:|||:|:|||||||||||: |||||||||||||||||||| || |
Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
              |::|:| |||||||||||||||||||||| |||||:|||||||||||||||||||||||
Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRAVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
              |||||||| ||| | |::  : ::||| |:|::|   | |    |  |||||||| |
Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
              ||:|||||||||||||||||||  | ||::| |||||:||||||||||||||||||||
```

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Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
             |||||||||| |||||||||||||||||||||||||||||||| ||:|| :|| ||||
Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
              ||::|| |||||||||||||||| |  |||  |||:|: :|||||::|| :||:||||
Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
                |||||||||||||| |:::|:||| ||||||||||||||||||:||||||||||
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
              |||||||||||||||||||||:||||:|||||| | |||||||:|| |||:||||||
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
              |||||||||:||||:||| |||    :   | :||||:|:||| || :|||||||:|:|||
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
              ||:|||||||||||| |||||||:||||:||||||:||||||:: |||||||   || |
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
              ||||:: || |||||||||||||:|||||||||||||||||||:|||||:|||:||||:
Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
              |||||||||:|| |||||::||||:||:||:: :|  | :::: |     :  | :|
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
              :   ::|| :    |  :    ||: |||||||:   :  :    | |  ||
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995
```

RESULT 29
ADB78604
ID ADB78604 standard; protein; 2005 AA.
XX
AC ADB78604;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:148.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78643.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 148; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 60.9%; Score 6392.5; DB 7; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;
Matches 1300; Conservative 233; Mismatches 359; Indels 201; Gaps 33;

```
Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||:|:||::|:     :: |:   :|  |:|  ||:| | |
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              | :||: | |::  |||||||:|  :|||||||||| | ||||| |||:|:||:|||: |
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||||||||||||||||||   :|| ||| |||||| |||||||:|||||||||
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||:||  || |||||||||||||||||||||||||||| ||||||||||
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
              ||||||:|||:|||||||||||||||||||:||::          | |:    | |:
Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
              : :|  :       : | |: |  ::    | :| |||||||||| ||||| |:||| ||
Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
              ::||||||:|:||||:|||||||| || ||| |||:||| |||||:||||||||||:|||
Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR----------------GV 453
              |||||||||||||: | |:||  ||: :| |||: |                     |:
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```
Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAAASAESRDFSGAGGI 480

Qy        454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504

Db        481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy        505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549

Db        540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy        550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606

Db        600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy        607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666

Db        659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy        667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726

Db        709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy        727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786

Db        769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy        787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846

Db        829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy        847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904

Db        889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964

Db        949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017

Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS----------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050

Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110

Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170

Db       1146 ---------VDIGAPAEGEQPE----------VEPEESLE----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230

Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290

Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350

Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407

Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467

Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527

Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587

Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNIVYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647

Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707

Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766

Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826

Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886

Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946

Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999

Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKPE---KDKSEKED 1995
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RESULT 30
ADB78603
ID   ADB78603 standard; protein; 2005 AA.
XX
AC   ADB78603;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:147.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
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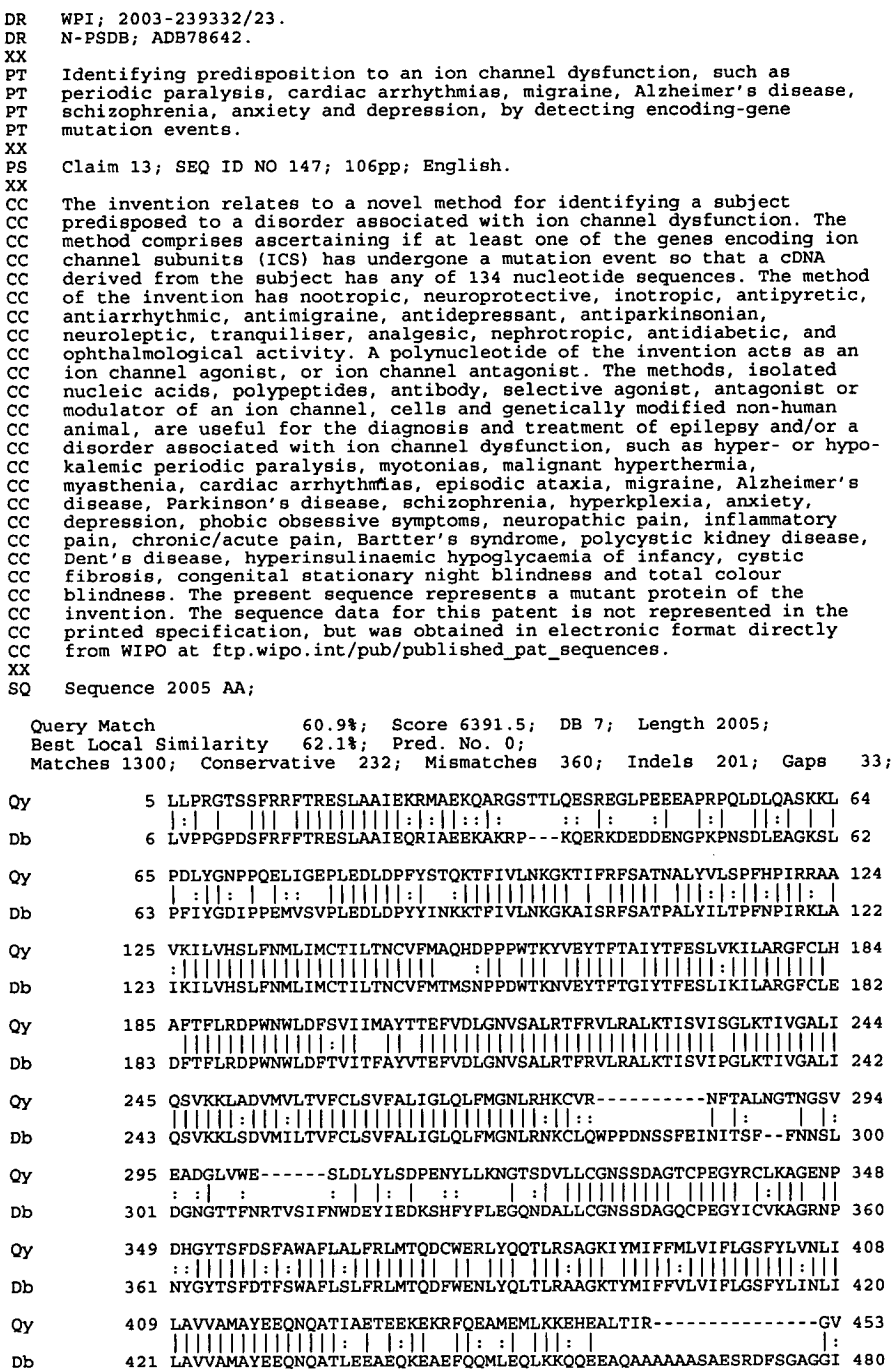
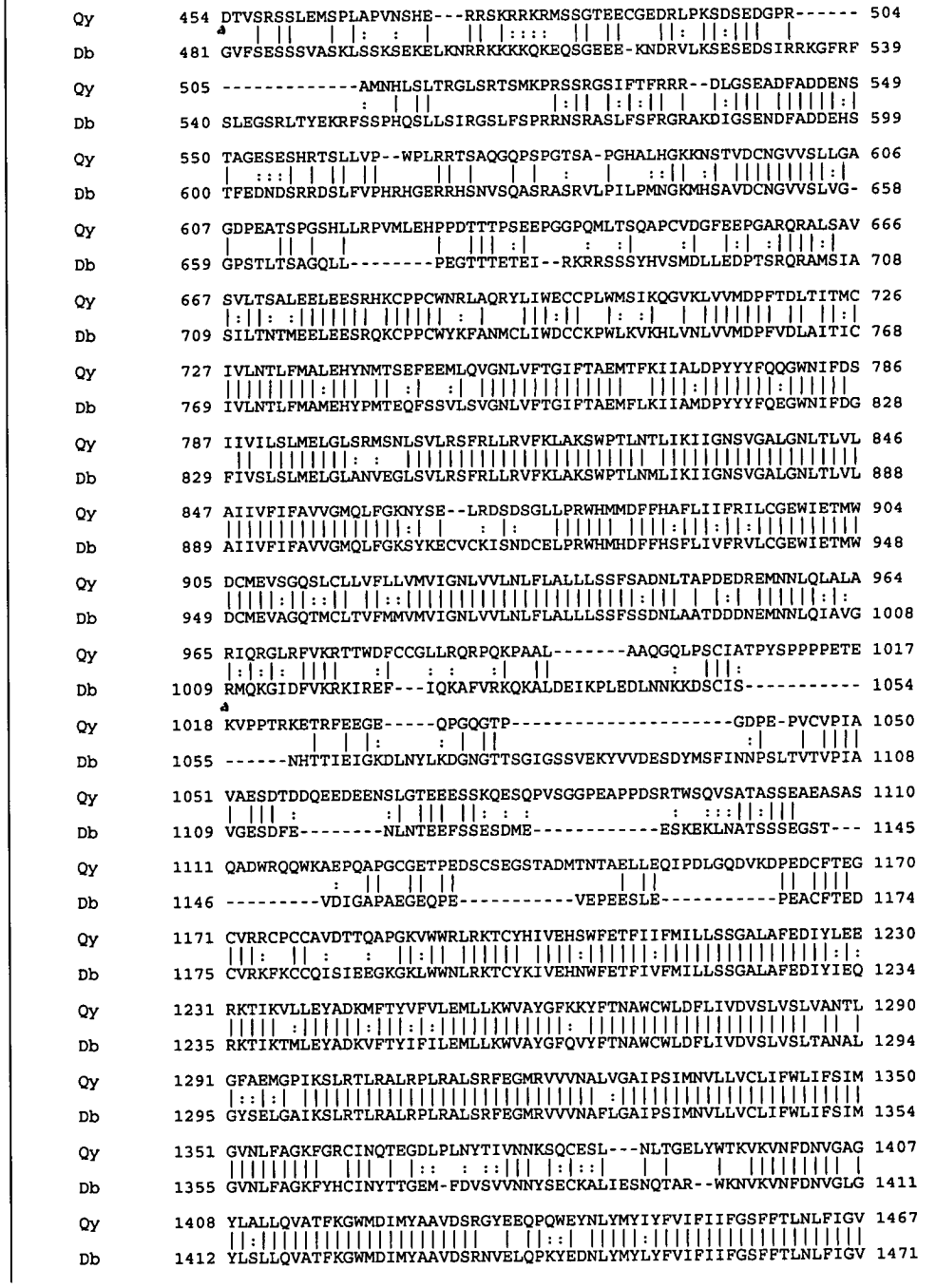
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78642.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 147; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 60.9%; Score 6391.5; DB 7; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;
Matches 1300; Conservative 232; Mismatches 360; Indels 201; Gaps 33;





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Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995
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RESULT 31
ADB78605
ID   ADB78605 standard; protein; 2005 AA.
XX
AC   ADB78605;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:149.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
DR   N-PSDB; ADB78644.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 13; SEQ ID NO 149; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
CC   nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC   modulator of an ion channel, cells and genetically modified non-human
CC   animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC   disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC   kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC   myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC   disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC   depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC   pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC   Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC   fibrosis, congenital stationary night blindness and total colour
CC   blindness. The present sequence represents a mutant protein of the
CC   invention. The sequence data for this patent is not represented in the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ   Sequence 2005 AA;
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Query Match 60.9%; Score 6391.5; DB 7; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;
Matches 1300; Conservative 232; Mismatches 360; Indels 201; Gaps 33;

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Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR----------------GV 453
Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAASAESRDFSGAGGI 480
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Qy       454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
Db       481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy       505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
Db       540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy       550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
Db       600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy       607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
Db       659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy       667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
Db       709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy       727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
Db       769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy       787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
Db       829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy       847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
Db       889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy       905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
Db       949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy       965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
Db      1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS----------- 1054

Qy      1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
Db      1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy      1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
Db      1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy      1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
Db      1146 ---------VDIGAPAEGEQPE-----------VEPEESLE-----------PEACFTED 1174

Qy      1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
Db      1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy      1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
Db      1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy      1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
Db      1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy      1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
Db      1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy      1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
Db      1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy      1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
Db      1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy      1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
Db      1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy      1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
Db      1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy      1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
Db      1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy      1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
Db      1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy      1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
Db      1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFVDALDPPLLI 1831

Qy      1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
Db      1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy      1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
Db      1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy      1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
Db      1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995
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RESULT 32
ADC46947
ID   ADC46947 standard; protein; 2005 AA.
XX
AC   ADC46947;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human SCN2A amino acid sequence #SEQ ID 3.
XX
KW   SCN2A; voltage-gated ion channel; human; neuroprotective; gene therapy;
KW   vaccine; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO2003060525-A1.
XX
PD   24-JUL-2003.
XX
PF   16-JAN-2003; 2003WO-EP000400.
XX
PR   17-JAN-2002; 2002EP-00001236.
PR   17-JAN-2002; 2002US-0348674P.
XX
PA   (EVOT-) EVOTEC NEUROSCIENCES GMBH.
XX
PI   Hipfel R,  Von Der Kammer H,  Pohlner J;
XX
DR   WPI; 2003-598580/56.
DR   N-PSDB; ADC46961.
XX
PT   Diagnosing or prognosticating a neurodegenerative disease by detecting
PT   the level or activity of transcription or translation products of the
PT   gene coding for the voltage-gated ion channel SCN2A.
XX
PS   Disclosure; Fig 9; 67pp; English.
XX
```

CC The invention relates to a method for diagnosing or prognosticating a
CC neurodegenerative disease in a subject, or determining whether a subject
CC is at increased risk of developing the disease. The method comprises
CC detecting the level and/or activity of a transcription or translation
CC product of the gene coding for the voltage-gated ion channel SCN2A. The
CC modulator of an activity and/or of a level of at least one substance is
CC useful for preparing a composition for treating or preventing a
CC neurodegenerative disease, in particular Alzheimer's disease. The current
CC sequence represents the human SCN2A amino acid sequence.
XX
SQ Sequence 2005 AA;

Query Match 60.9%; Score 6391.5; DB 7; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;
Matches 1300; Conservative 232; Mismatches 360; Indels 201; Gaps 33;

```
Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| ||||||||||:|:||::|:     :: |:   :|  |:|  ||:| | |
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              | :||: | |::  |||||||:|  :||||||||| | ||||| |||:|:||:|||: |
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||||||||||||||||    :|| ||| |||||| |||||||:|||||||||
Db        123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||:||  || |||||||||||||||||||||||||||| ||||||||||
Db        183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
              ||||||:|||:|||||||||||||||||||:||::          | |:    | |:
Db        243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy        295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
              : :|  :       : | |: |  ::    | :| |||||||||| ||||| |:||| ||
Db        301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy        349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
              ::||||||:|:||||:|||||||| || ||| |||:||| |||||:|||||||||:|||
Db        361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy        409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR--------------GV 453
              |||||||||||||: | |:||  ||: :| |||: |                    |:
Db        421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAAASAESRDFSGAGGI 480

Qy        454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
                | ||   | |:  :  |   || |:::  || ||   ||: ||:||| |
Db        481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy        505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
                         :  | ||          |:|| |:|:|| |  |:||| ||||||:|
Db        540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy        550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
              |  :::| | || ||     || |   | |  :   |   ::|| :| |||||||||:|
Db        600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy        607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
              |    || | |          |  ||| :|     :  :|    :|  |:| :||||:|
Db        659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy        667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
              |:||: :||||||| |||||| : |    |||:||  |: :|  | |||||| || ||:|
Db        709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy        727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db        769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy        787 IIVILSLMELGLSRMSNLSVLRSFRLLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
              || ||||||||: :  |||||||||||||||||||||||||| |||||||||||||||||
Db        829 FIVSLSLMELGLANVEGLSVLRSFRLLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy        847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
              |||||||||||||||||:| |  : |:   |||||| |||||||:|||||||||||||||
Db        889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
              |||||:||::|| ||::|||||||||||||||||||:||| | |:| |||||:|:
Db        949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
              |:|:|: ||||   :|   : :   :|  ||          :  |||:
Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
                      |  | |:     : | ||                    :|   | ||||
Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
              | ||| :        :| ||| ||: : :                 :  :::||:|||
Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
                    :  ||  || ||              | ||           || ||||
Db       1146 ---------VDIGAPAEGEQPE----------VEPEESLE----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
              |||:  || :   :  ||:|| |||||  |||||:||||||||||||||||||||:|:
Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
              ||||| :||||||:|||:|:|||||||||||: |||||||||||||||||||| || |
Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
              |::|:| |||||||||||||||||||||||| |||||:|||||||||||||||||||||
Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRAVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
              |||||||| ||| | |::  : ::||| |:|::|   | |    | |||||||| |
Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
              ||:|||||||||||||||||  | ||::| |||||:||||||||||||||||||||||
Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
              |||||||||| ||||||||||||||||||||||||||||||||||| ||:|| :|| ||||
Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
              ||::|| ||||||||||||||||| |  |||  |||:|: :|||||::|| :||:||||
Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
                |||||||||||||  |:::|:||| |||||||||||||||||:||||||||||
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
              |||||||||||||||||||||:||||:|||||| | ||||||||:|| |||:||||||
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
              |||||||||:||||:||| |||    :    | :||||:|:||| || :|||||||:|:|||
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
              ||:|||||||||||| ||||||||:||||:||||||:|||||:: |||||||  || |
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
              ||||:: || ||||||||||||:|||||||||||||||||||:|||||:|||:||||:
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Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
              |||||||||:|| ||||||::||||:||:||:: :|  | :::: |    :  | :|
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
              :  ::|| :    |  :    ||: ||||||||:   : :    | |  ||
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995


RESULT 33
ADS52265
ID   ADS52265 standard; protein; 2005 AA.
XX
AC   ADS52265;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Human sodium channel type II (SCN2A) protein SeqID60.
XX
KW   sodium channel type II; SCN2A; mutation; mis-sense; nonsense;
KW   frame shift; splice site; obstinacy childhood epilepsy; mental illness;
KW   human.
XX
OS   Homo sapiens.
XX
PN   JP2004275115-A.
XX
PD   07-OCT-2004.
XX
PF   18-MAR-2003; 2003JP-00072979.
XX
PR   18-MAR-2003; 2003JP-00072979.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA   (KOKU-) KOKURITSU RYOYOJO SHIZUOKA SHINKEI IRYO.
XX
DR   WPI; 2004-712375/70.
DR   N-PSDB; ADS52206.
XX
PT   Novel isolated human sodium channel type II SCN2A gene, its cDNA or mRNA
PT   having disease mutation e.g., mis-sense, nonsense, frame shift or
PT   splicing site mutation, useful as primer or probe for detecting obstinacy
PT   childhood epilepsy.
XX
PS   Disclosure; SEQ ID NO 60; 59pp; Japanese.
XX
CC   This invention relates to a novel isolated human sodium channel type II
CC   (SCN2A) gene, its corresponding cDNA or mRNA, having a disease mutation
CC   (mis-sense, nonsense, frame shift, splicing site mutation) in the DNA
CC   which encodes the human SCN2A protein. The invention enables diagnosis of
CC   obstinacy childhood epilepsy accompanying regression of serious mental
CC   illness, by detection of a mutation in a gene, and thus contributes to
CC   the development of treatment methods. The present sequence is that of the
CC   protein encoded by the human sodium channel type II (SCN2A) gene of the
CC   invention.
XX
SQ   Sequence 2005 AA;

  Query Match             60.9%;  Score 6391.5;  DB 8;  Length 2005;
  Best Local Similarity   62.1%;  Pred. No. 0;
  Matches 1300;  Conservative  232;  Mismatches  360;  Indels  201;  Gaps   33;

Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||:|:||::|:     :: |:   :|  |:|  ||:| | |
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              | :||: | |::  |||||||:|  :|||||||||| | ||||| |||:|:||:|||: |
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
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Db       123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy       185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||:||  || ||||||||||||||||||||||||||||| ||||||||||
Db       183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy       245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
              ||||||:|||:||||||||||||||||||||:||::          | |:    | |:
Db       243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy       295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
              : :|  :       : | |: |  ::    | :| |||||||||| ||||| |:||| ||
Db       301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy       349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
              ::||||||:|:||||:||||||| || ||| |||:||| |||||:|||||||||:|||
Db       361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy       409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR--------------GV 453
              |||||||||||||: | |:||  ||: :| |||: |                    |:
Db       421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAASAESRDFSGAGGI 480

Qy       454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
                | ||   | |:  :  |   || |::::  || ||   ||: ||:||| |
Db       481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy       505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
                         :  | ||           |:|| |:|:|| |  |:||| ||||||:|
Db       540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy       550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
              |  :::| | || ||     || |  | |  :   |   ::|| :| ||||||||:|
Db       600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy       607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
              |    || |  |          |  ||| :|     :  :|    :|  |:| :||||:|
Db       659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy       667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
              |:||: :|||||| |||||| : |   |||:||  |: :|  | ||||||| || ||:|
Db       709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy       727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db       769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy       787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
              || |||||||: :  |||||||||||||||||||| ||||||||||||||||||||
Db       829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy       847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
              |||||||||||||||:| |   : |:   |||||| ||||:|||:||:|||||||||||
Db       889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy       905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
              |||||:||::|| ||::|||||||||||||||||||||:||| | |:| ||||||:|:
Db       949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy       965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
              |:|:|: ||||   :|   : :   :|  ||             :  |||:
Db      1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS----------- 1054

Qy      1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
                  | | |:      : | ||                      :|   | ||||
Db      1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy      1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
              | ||| :        :| ||| ||: : :              :  :::||:|||
Db      1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy      1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
                    :  ||  || ||                | ||           || ||||
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Db       1146 ---------VDIGAPAEGEQPE-----------VEPEESLE-----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
              |||:  || :   :  ||:|| |||||| ||||:||||||:||||||||||||||||:|: 
Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
              ||||| :|||||:|||:|:|||||||||||: |||||||||||||||||||||| || | 
Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
              |::|:| |||||||||||||||||||||| |||||:|||||||||||||||||||||||| 
Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRAVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
              ||||||||  ||| | |::  : ::||| |:|::|   | |    |  |||||||| | 
Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
              ||:|||||||||||||||||||  | ||::| |||||:|||||||||||||||||||||| 
Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
              |||||||||| |||||||||||||||||||||||||||||| ||:|| :|| |||| 
Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
               ||::|| |||||||||||||||| |  |||  |||:|: :|||||::|| :||:|||| 
Db       1532 VFDISIMILILCLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
               ||||||||||||||  |:::|:||| ||||||||||||||||:|||||||||| 
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
              |||||||||||||||||||:||||:|||||| | ||||||||:|| |||:|||||| 
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
              |||||||||:||||:||| |||   :   | :||||:|:||| || :|||||||:|:||| 
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
              ||:|||||||||||| |||||||:||||:|||||:|||||:: |||||||  || | 
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
              ||||:: || |||||||||||:||||||||||||||||:|||||:|||:||||: 
Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
              |||||||||:|| |||||::||||:||:||:: :|  | ::::  |     :  | :| 
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949

Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
              :   ::|| :    |  :    ||: ||||||||:   :  :    | |  || 
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995


RESULT 34
ADY27151
ID   ADY27151 standard; protein; 2005 AA.
XX
AC   ADY27151;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human SCN2A variant R223Q.
XX
KW   SCN2A; anticonvulsant; muscular-Gen.; neuroprotective; antiarrhythmic;
KW   antimigraine; nootropic; antiparkinsonian; neuroleptic; tranquilizer;
KW   antidepressant; analgesic; nephrotropic; antidiabetic; cytostatic;
KW   diagnostic; anxiety disorder; major depressive disorder; epilepsy;
KW   paralysis; hyperthermia; myasthenia gravis; heart arrhythmia; ataxia;
KW   migraine; Alzheimers disease; Parkinsons disease; cystic fibrosis; pain;
KW   inflammation; polycystic kidney disease; phobia; schizophrenia;
KW   neuropathic pain; hyperglycemia; hyperinsulinemia; sodium channel;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1319
FT                   /label= R1319Q
FT                   /note= "wild-type Arg substituted with Gln"
XX
PN   WO2005014863-A1.
XX
PD   17-FEB-2005.
XX
PF   06-AUG-2004; 2004WO-AU001051.
XX
PR   07-AUG-2003; 2003AU-00904154.
XX
PA   (BION-) BIONOMICS LTD.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE,  Davy A;
XX
DR   WPI; 2005-195767/20.
DR   N-PSDB; ADY27079.
XX
PT   Identifying subject predisposed to disorder associated with ion channel
PT   dysfunction, involves determining presence of specific mutation event in
PT   genes encoding ion channel subunits.
XX
PS   Claim 20; SEQ ID NO 87; 347pp; English.
XX
CC   This invention describes a novel method of identifying a subject
CC   predisposed to disorder associated with ion channel dysfunction
CC   comprising ascertaining whether at least one of the genes encoding ion
CC   channel subunits in the subject has undergone a mutation. The invention
CC   also describes 1) isolated nucleic acid molecules encoding an isolated
CC   polypeptide which is a mutant or variant ion channel subunit (including a
CC   mutant KCNQ2 subunit, where the mutation event has occurred in C terminal
CC   domain of the subunit and leads to disturbance in the calmodulin binding
CC   affinity of the subunit) and 2) an expression vector, cells, antibodies
CC   and a method for producing a non-human transgenic animal which are all
CC   used for screening of candidate pharmaceutical agents for diagnosing or
CC   treating epilepsy or a disorder associated with ion channel dysfunction.
CC   The mutation detected in the method disrupts the functioning of an
CC   assembled ion channel so as to produce an epilepsy phenotype in the
CC   subject or produces one or more disorders associated with ion channel
CC   dysfunction such as hyper- or hypo-kalemic periodic paralysis, myotonias,
CC   malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,
CC   migraine, Alzheimer's disease, Parkinson's disease, schizophrenia,
CC   anxiety, depression, phobic obsessive symptoms, neuropathic pain,
CC   inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic
CC   kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy,
CC   cystic fibrosis, congenital stationary night blindness and total color-
CC   blindness in the subject or to produce an epilepsy phenotype when
CC   expressed in combination with one or more additional mutations or
CC   variations in the ion channel subunit genes. The products of the
CC   invention have anticonvulsant, muscular-Gen., neuroprotective,
CC   antiarrhythmic, antimigraine, nootropic, antiparkinsonian, neuroleptic,
CC   tranquilizer, antidepressant, analgesic, nephrotropic, antidiabetic and
CC   cytostatic activity. This sequence represents a fragment of the human
CC   sodium ion channel subunit SCN2A encoded by exon 20 which contains the
CC   mutation R1319Q.
XX
SQ   Sequence 2005 AA;

  Query Match             60.9%;  Score 6391.5;  DB 9;  Length 2005;
  Best Local Similarity   62.1%;  Pred. No. 0;
  Matches 1300;  Conservative  233;  Mismatches  359;  Indels  201;  Gaps   33;
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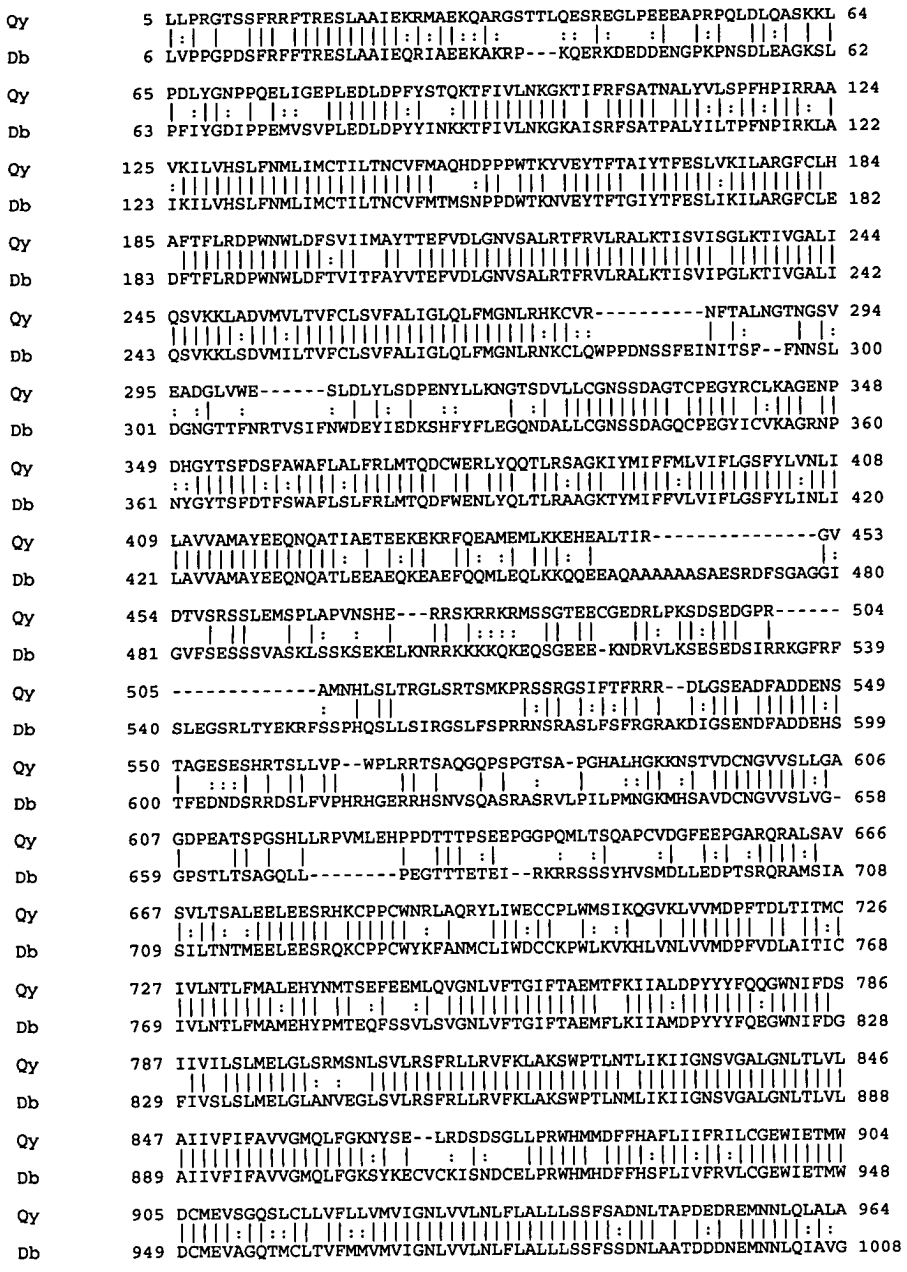

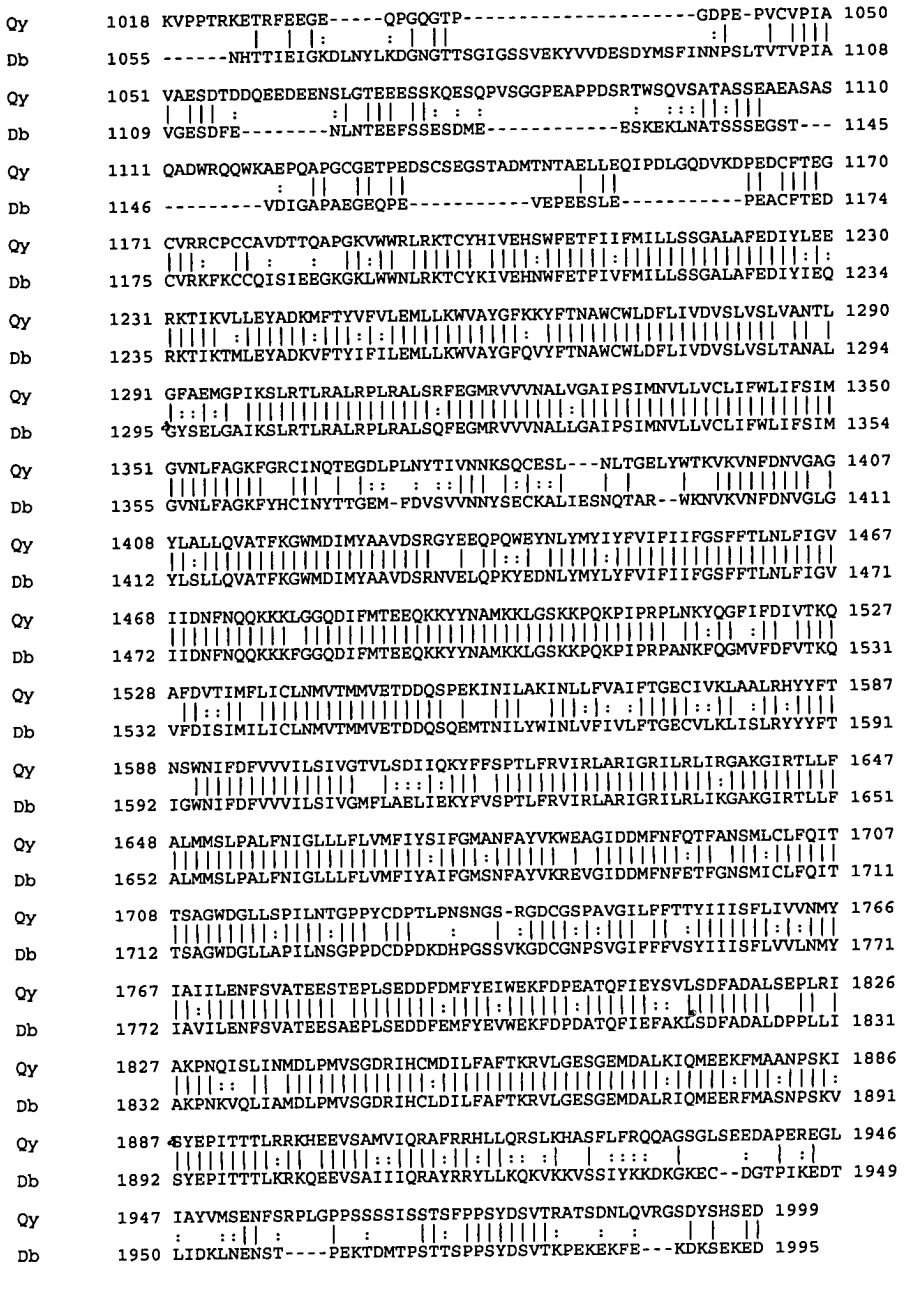

RESULT 35
ADY27150
ID ADY27150 standard; protein; 2005 AA.
XX

AC ADY27150;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human SCN2A variant R223Q.
XX
KW SCN2A; anticonvulsant; muscular-Gen.; neuroprotective; antiarrhythmic;
KW antimigraine; nootropic; antiparkinsonian; neuroleptic; tranquilizer;
KW antidepressant; analgesic; nephrotropic; antidiabetic; cytostatic;
KW diagnostic; anxiety disorder; major depressive disorder; epilepsy;
KW paralysis; hyperthermia; myasthenia gravis; heart arrhythmia; ataxia;
KW migraine; Alzheimers disease; Parkinsons disease; cystic fibrosis; pain;
KW inflammation; polycystic kidney disease; phobia; schizophrenia;
KW neuropathic pain; hyperglycemia; hyperinsulinemia; sodium channel;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1200
FT /label= T1200A
FT /note= "wild-type Thr substituted with Ala"
XX
PN WO2005014863-A1.
XX
PD 17-FEB-2005.
XX
PF 06-AUG-2004; 2004WO-AU001051.
XX
PR 07-AUG-2003; 2003AU-00904154.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE, Davy A;
XX
DR WPI; 2005-195767/20.
DR N-PSDB; ADY27078.
XX
PT Identifying subject predisposed to disorder associated with ion channel
PT dysfunction, involves determining presence of specific mutation event in
PT genes encoding ion channel subunits.
XX
PS Claim 20; SEQ ID NO 86; 347pp; English.
XX
CC This invention describes a novel method of identifying a subject
CC predisposed to disorder associated with ion channel dysfunction
CC comprising ascertaining whether at least one of the genes encoding ion
CC channel subunits in the subject has undergone a mutation. The invention
CC also describes 1) isolated nucleic acid molecules encoding an isolated
CC polypeptide which is a mutant or variant ion channel subunit (including a
CC mutant KCNQ2 subunit, where the mutation event has occurred in C terminal
CC domain of the subunit and leads to disturbance in the calmodulin binding
CC affinity of the subunit) and 2) an expression vector, cells, antibodies
CC and a method for producing a non-human transgenic animal which are all
CC used for screening of candidate pharmaceutical agents for diagnosing or
CC treating epilepsy or a disorder associated with ion channel dysfunction.
CC The mutation detected in the method disrupts the functioning of an
CC assembled ion channel so as to produce an epilepsy phenotype in the
CC subject or produces one or more disorders associated with ion channel
CC dysfunction such as hyper- or hypo-kalemic periodic paralysis, myotonias,
CC malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,
CC migraine, Alzheimer's disease, Parkinson's disease, schizophrenia,
CC anxiety, depression, phobic obsessive symptoms, neuropathic pain,
CC inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic
CC kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy,
CC cystic fibrosis, congenital stationary night blindness and total color-
CC blindness in the subject or to produce an epilepsy phenotype when
CC expressed in combination with one or more additional mutations or
CC variations in the ion channel subunit genes. The products of the
CC invention have anticonvulsant, muscular-Gen., neuroprotective,
CC antiarrhythmic, antimigraine, nootropic, antiparkinsonian, neuroleptic,
CC tranquilizer, antidepressant, analgesic, nephrotropic, antidiabetic and
CC cytostatic activity. This sequence represents a fragment of the human
CC sodium ion channel subunit SCN2A encoded by exon 19 which contains the
CC mutation T1200A.
XX
SQ Sequence 2005 AA;

Query Match 60.9%; Score 6390.5; DB 9; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;
Matches 1300; Conservative 232; Mismatches 360; Indels 201; Gaps 33;

```
Qy    5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
Db    6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy   65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
Db   63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy  125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
Db  123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy  185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
Db  183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 242

Qy  245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
Db  243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy  295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
Db  301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy  349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
Db  361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy  409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR----------------GV 453
Db  421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAASAESRDFSGAGGI 480

Qy  454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
Db  481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy  505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
Db  540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy  550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
Db  600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy  607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
Db  659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy  667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
Db  709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy  727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
Db  769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy  787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
Db  829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy  847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
```

```
Db        889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy        905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
              |||||:||::|| ||::|||||||||||||||||||||||:||| | |:| ||||||:|:
Db        949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy        965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
              |:|:|: |||| :|  : :  :|  ||       :  |||:
Db       1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054

Qy       1018 KVPPTRKETRFEEGE-----QPGQGTP--------------------GDPE-PVCVPIA 1050
                    |  | |:     : | ||                     :|   | ||||
Db       1055 ------NHTTIEIGKDLNYLKDGNGTTSGIGSSVEKYVVDESDYMSFINNPSLTVTVPIA 1108

Qy       1051 VAESDTDDQEEDEENSLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASAS 1110
              | ||| :         :| ||| ||: : :          :  :::||:|||
Db       1109 VGESDFE--------NLNTEEFSSESDME-----------ESKEKLNATSSSEGST--- 1145

Qy       1111 QADWRQQWKAEPQAPGCGETPEDSCSEGSTADMTNTAELLEQIPDLGQDVKDPEDCFTEG 1170
                    :  ||  || ||           | ||           || ||||
Db       1146 ---------VDIGAPAEGEQPE-----------VEPEESLE-----------PEACFTED 1174

Qy       1171 CVRRCPCCAVDTTQAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEE 1230
              |||:  || :   :  ||:|| ||| || ||||:||||||:||||||||||||||||:|:
Db       1175 CVRKFKCCQISIEEGKGKLWWNLRKACYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQ 1234

Qy       1231 RKTIKVLLEYADKMFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTL 1290
              ||||| :|||||:|||:|:|||||||||||||: |||||||||||||||||||| || |
Db       1235 RKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQVYFTNAWCWLDFLIVDVSLVSLTANAL 1294

Qy       1291 GFAEMGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIM 1350
              |::|:| ||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db       1295 GYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIMNVLLVCLIFWLIFSIM 1354

Qy       1351 GVNLFAGKFGRCINQTEGDLPLNYTIVNNKSQCESL---NLTGELYWTKVKVNFDNVGAG 1407
              |||||||||  ||| | |::  : ::||| |:|::|   | |    |  |||||||| |
Db       1355 GVNLFAGKFYHCINYTTGEM-FDVSVVNNYSECKALIESNQTAR--WKNVKVNFDNVGLG 1411

Qy       1408 YLALLQVATFKGWMDIMYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGV 1467
              ||:|||||||||||||||||||  | ||::| |||||:|||||||||||||||||||||
Db       1412 YLSLLQVATFKGWMDIMYAAVDSRNVELQPKYEDNLYMYLYFVIFIIFGSFFTLNLFIGV 1471

Qy       1468 IIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQ 1527
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Db       1472 IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQ 1531

Qy       1528 AFDVTIMFLICLNMVTMMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFT 1587
               ||:|| |||||||||||||||| |  |||  |||:|: :|||||::|| :||:||||
Db       1532 VFDISIMILICLNMVTMMVETDDQSQEMTNILYWINLVFIVLFTGECVLKLISLRYYYFT 1591

Qy       1588 NSWNIFDFVVVILSIVGTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLF 1647
                |||||||||||||  |:::|:||| |||||||||||||||||:|||||||||
Db       1592 IGWNIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLF 1651

Qy       1648 ALMMSLPALFNIGLLLFLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQIT 1707
              |||||||||||||||||||:||||:|||||| | ||||||||:|| |||:||||||
Db       1652 ALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQIT 1711

Qy       1708 TSAGWDGLLSPILNTGPPYCDPTLPNSNGS-RGDCGSPAVGILFFTTYIIISFLIVVNMY 1766
              |||||||||:||||:||| |||    :   | :||||:|:||| || :||||||:|:|||
Db       1712 TSAGWDGLLAPILNSGPPDCDPDKDHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVLNMY 1771

Qy       1767 IAIILENFSVATEESTEPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRI 1826
              ||:|||||||||||| |||||||:||||:||||||:|||||:: |||||||  || |
Db       1772 IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAKLSDFADALDPPLLI 1831

Qy       1827 AKPNQISLINMDLPMVSGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKI 1886
              ||||:: || |||||||||||||:||||||||||||||||||:|||||:|||:||||:
Db       1832 AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKV 1891

Qy       1887 SYEPITTTLRRKHEEVSAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGL 1946
              |||||||||:|| ||||||::||||:||:||::: :|  | :::: |     :  | :|
Db       1892 SYEPITTTLKRKQEEVSAIIIQRAYRRYLLKQKVKKVSSIYKKDKGKEC--DGTPIKEDT 1949
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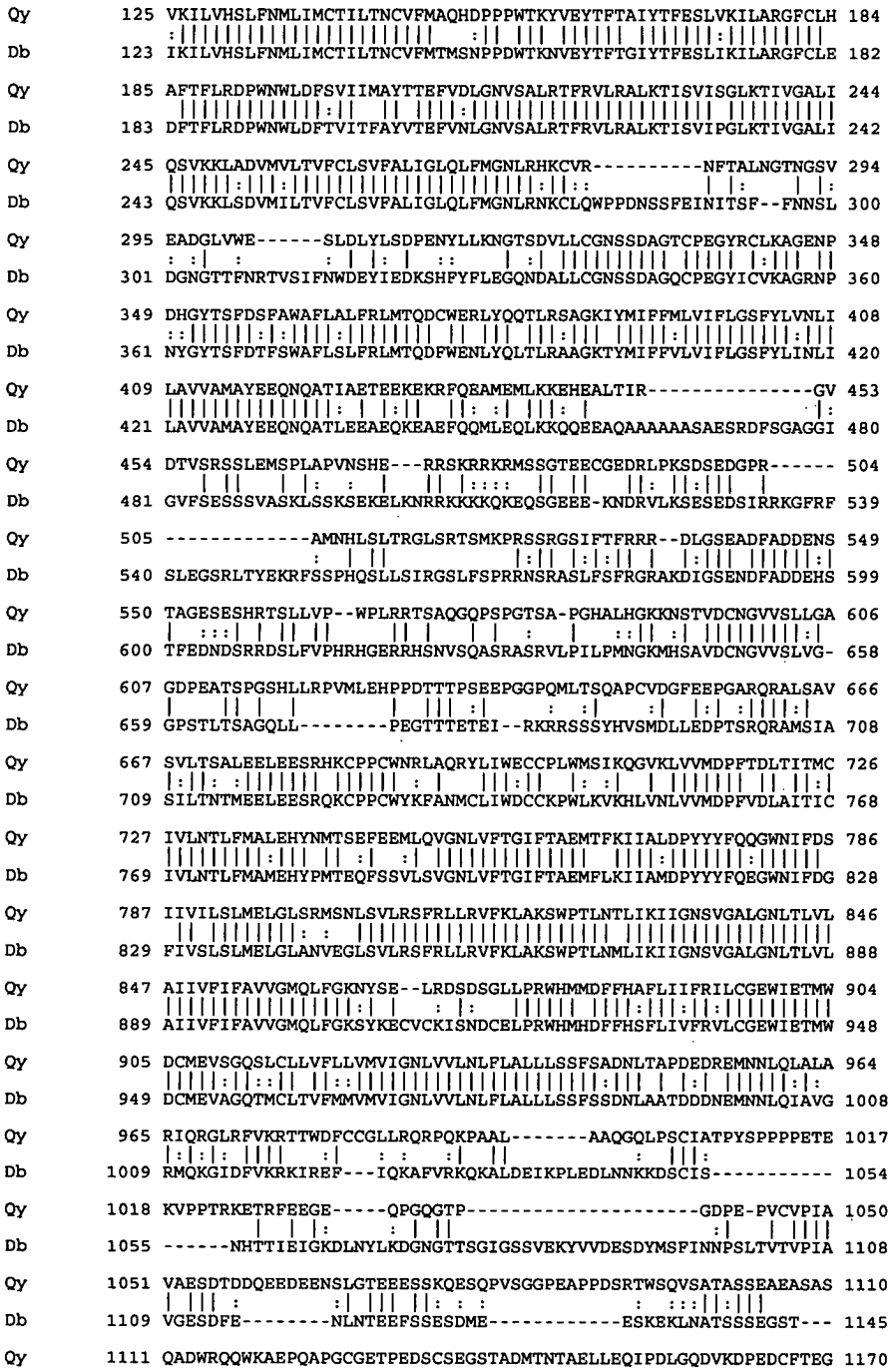
Qy       1947 IAYVMSENFSRPLGPPSSSSISSTSFPPSYDSVTRATSDNLQVRGSDYSHSED 1999
              :   ::|| :    |  :    ||: ||||||||:   :  :    | |  ||
Db       1950 LIDKLNENST----PEKTDMTPSTTSPPSYDSVTKPEKEKFE---KDKSEKED 1995

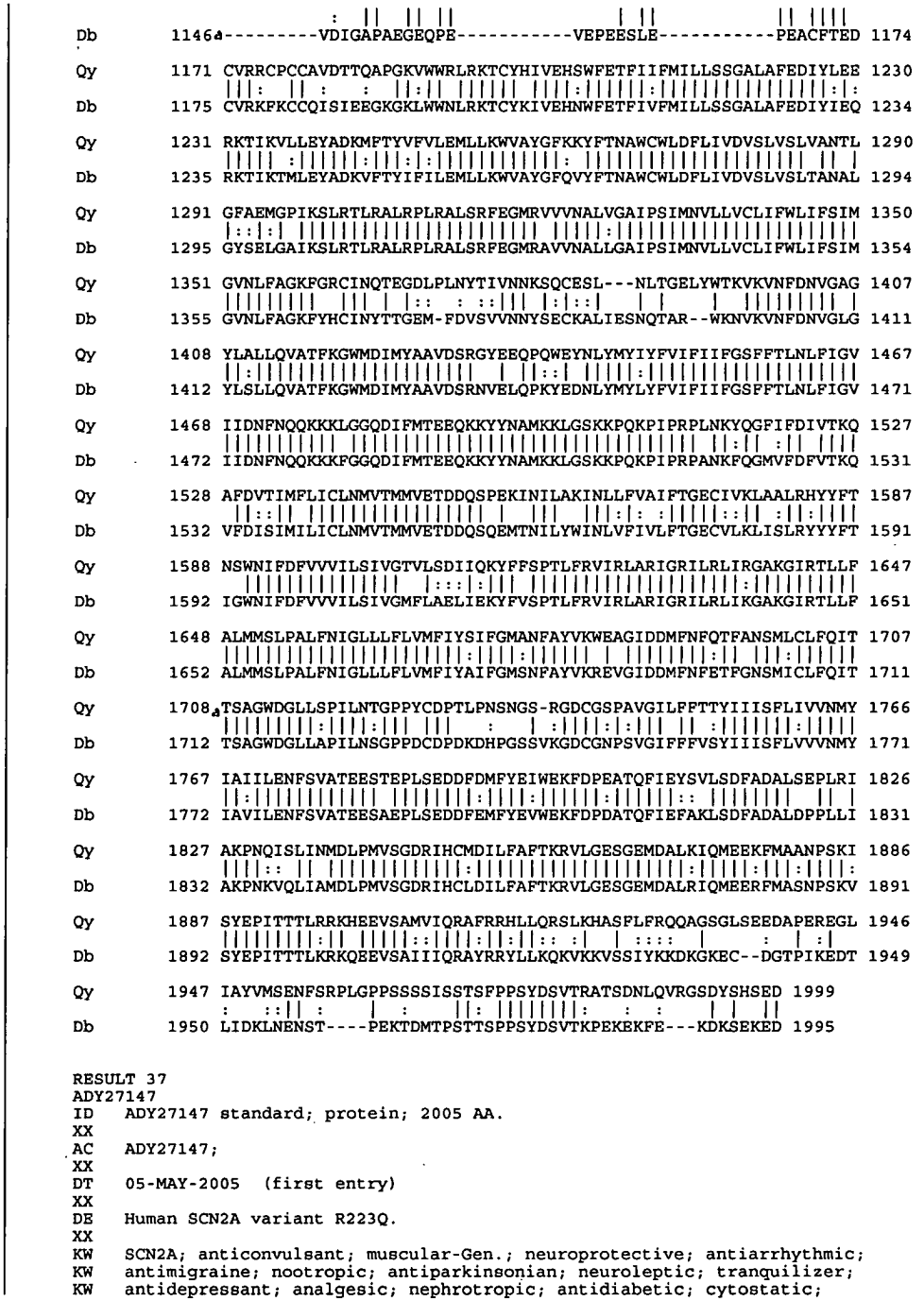

RESULT 36
AAB99677
ID   AAB99677 standard; protein; 2005 AA.
XX
AC   AAB99677;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA001404.
XX
PR   26-NOV-1999;   99US-0167623P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  Lafreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   N-PSDB; AAH55794.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT   variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS   Disclosure; Page 131-138; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The method
CC   comprises determining the genotype of at least one gene selected from
CC   SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC   shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC   channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC   q31. Compounds identified as modulators of the biological activity of
CC   SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC   or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC   represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC   oligonucleotides and proteins given in the exemplification of the present
CC   invention
XX
SQ   Sequence 2005 AA;

  Query Match             60.9%;  Score 6389.5;  DB 4;  Length 2005;
  Best Local Similarity   62.1%;  Pred. No. 0;
  Matches 1300;  Conservative  232;  Mismatches  360;  Indels  201;  Gaps   33;

Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||||:|:||::|:     :: |:   :|  |:|  ||:| | |
Db          6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
               | :||: | |::  |||||||:|  :|||||||||| | ||||| |||:|:||:|||: |
Db         63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122
```





RESULT 37
ADY27147
ID ADY27147 standard; protein; 2005 AA.
XX
AC ADY27147;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human SCN2A variant R223Q.
XX
KW SCN2A; anticonvulsant; muscular-Gen.; neuroprotective; antiarrhythmic;
KW antimigraine; nootropic; antiparkinsonian; neuroleptic; tranquilizer;
KW antidepressant; analgesic; nephrotropic; antidiabetic; cytostatic;

KW diagnostic; anxiety disorder; major depressive disorder; epilepsy;
KW paralysis; hyperthermia; myasthenia gravis; heart arrhythmia; ataxia;
KW migraine; Alzheimers disease; Parkinsons disease; cystic fibrosis; pain;
KW inflammation; polycystic kidney disease; phobia; schizophrenia;
KW neuropathic pain; hyperglycemia; hyperinsulinemia; sodium channel;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 223
FT /label= R223Q
FT /note= "wild-type Arg substituted with Gln"
XX
PN WO2005014863-A1.
XX
PD 17-FEB-2005.
XX
PF 06-AUG-2004; 2004WO-AU001051.
XX
PR 07-AUG-2003; 2003AU-00904154.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE, Davy A;
XX
DR WPI; 2005-195767/20.
DR N-PSDB; ADY27075.
XX
PT Identifying subject predisposed to disorder associated with ion channel
PT dysfunction, involves determining presence of specific mutation event in
PT genes encoding ion channel subunits.
XX
PS Claim 20; SEQ ID NO 83; 347pp; English.
XX
CC This invention describes a novel method of identifying a subject
CC predisposed to disorder associated with ion channel dysfunction
CC comprising ascertaining whether at least one of the genes encoding ion
CC channel subunits in the subject has undergone a mutation. The invention
CC also describes 1) isolated nucleic acid molecules encoding an isolated
CC polypeptide which is a mutant or variant ion channel subunit (including a
CC mutant KCNQ2 subunit, where the mutation event has occurred in C terminal
CC domain of the subunit and leads to disturbance in the calmodulin binding
CC affinity of the subunit) and 2) an expression vector, cells, antibodies
CC and a method for producing a non-human transgenic animal which are all
CC used for screening of candidate pharmaceutical agents for diagnosing or
CC treating epilepsy or a disorder associated with ion channel dysfunction.
CC The mutation detected in the method disrupts the functioning of an
CC assembled ion channel so as to produce an epilepsy phenotype in the
CC subject or produces one or more disorders associated with ion channel
CC dysfunction such as hyper- or hypo-kalemic periodic paralysis, myotonias,
CC malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,
CC migraine, Alzheimer's disease, Parkinson's disease, schizophrenia,
CC anxiety, depression, phobic obsessive symptoms, neuropathic pain,
CC inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic
CC kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy,
CC cystic fibrosis, congenital stationary night blindness and total color-
CC blindness in the subject or to produce an epilepsy phenotype when
CC expressed in combination with one or more additional mutations or
CC variations in the ion channel subunit genes. The products of the
CC invention have anticonvulsant, muscular-Gen., neuroprotective,
CC antiarrhythmic, antimigraine, nootropic, antiparkinsonian, neuroleptic,
CC tranquilizer, antidepressant, analgesic, nephrotropic, antidiabetic and
CC cytostatic activity. This sequence represents a fragment of the human
CC sodium ion channel subunit SCN2A encoded by exon 6A which contains the
CC mutation R223Q.
XX
SQ Sequence 2005 AA;

Query Match 60.9%; Score 6387.5; DB 9; Length 2005;
Best Local Similarity 62.1%; Pred. No. 0;

Matches 1299; Conservative 233; Mismatches 360; Indels 201; Gaps 33;

```
Qy    5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
Db    6 LVPPGPDSFRFFTRESLAAIEQRIAEEKAKRP---KQERKDEDDENGPKPNSDLEAGKSL 62

Qy   65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
Db   63 PFIYGDIPPEMVSVPLEDLDPYYINKKTFIVLNKGKAISRFSATPALYILTPFNPIRKLA 122

Qy  125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
Db  123 IKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 182

Qy  185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
Db  183 DFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTFRVLQALKTISVIPGLKTIVGVLI 242

Qy  245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTALNGTNGSV 294
Db  243 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPDNSSFEINITSF--FNNSL 300

Qy  295 EADGLVWE------SLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGENP 348
Db  301 DGNGTTFNRTVSIFNWDEYIEDKSHFYFLEGQNDALLCGNSSDAGQCPEGYICVKAGRNP 360

Qy  349 DHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNLI 408
Db  361 NYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI 420

Qy  409 LAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKKEHEALTIR----------------GV 453
Db  421 LAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAAAAAAASAESRDFSGAGGI 480

Qy  454 DTVSRSSLEMSPLAPVNSHE---RRSKRRKRMSSGTEECGEDRLPKSDSEDGPR------ 504
Db  481 GVFSESSSVASKLSSKSEKELKNRRKKKKQKEQSGEEE-KNDRVLKSESEDSIRRKGFRF 539

Qy  505 ------------AMNHLSLTRGLSRTSMKPRSSRGSIFTFRRR--DLGSEADFADDENS 549
Db  540 SLEGSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRASLFSFRGRAKDIGSENDFADDEHS 599

Qy  550 TAGESESHRTSLLVP--WPLRRTSAQGQPSPGTSA-PGHALHGKKNSTVDCNGVVSLLGA 606
Db  600 TFEDNDSRRDSLFVPHRHGERRHSNVSQASRASRVLPILPMNGKMHSAVDCNGVVSLVG- 658

Qy  607 GDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSAV 666
Db  659 GPSTLTSAGQLL--------PEGTTTETEI--RKRRSSSYHVSMDLLEDPTSRQRAMSIA 708

Qy  667 SVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITMC 726
Db  709 SILTNTMEELEESRQKCPPCWYKFANMCLIWDCCKPWLKVKHLVNLVVMDPFVDLAITIC 768

Qy  727 IVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFDS 786
Db  769 IVLNTLFMAMEHYPMTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDG 828

Qy  787 IIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLVL 846
Db  829 FIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL 888

Qy  847 AIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETMW 904
Db  889 AIIVFIFAVVGMQLFGKSYKECVCKISNDCELPRWHMHDFFHSFLIVFRVLCGEWIETMW 948

Qy  905 DCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLALA 964
Db  949 DCMEVAGQTMCLTVFMMVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG 1008

Qy  965 RIQRGLRFVKRTTWDFCCGLLRQRPQKPAAL-------AAQGQLPSCIATPYSPPPPETE 1017
Db 1009 RMQKGIDFVKRKIREF---IQKAFVRKQKALDEIKPLEDLNNKKDSCIS---------- 1054
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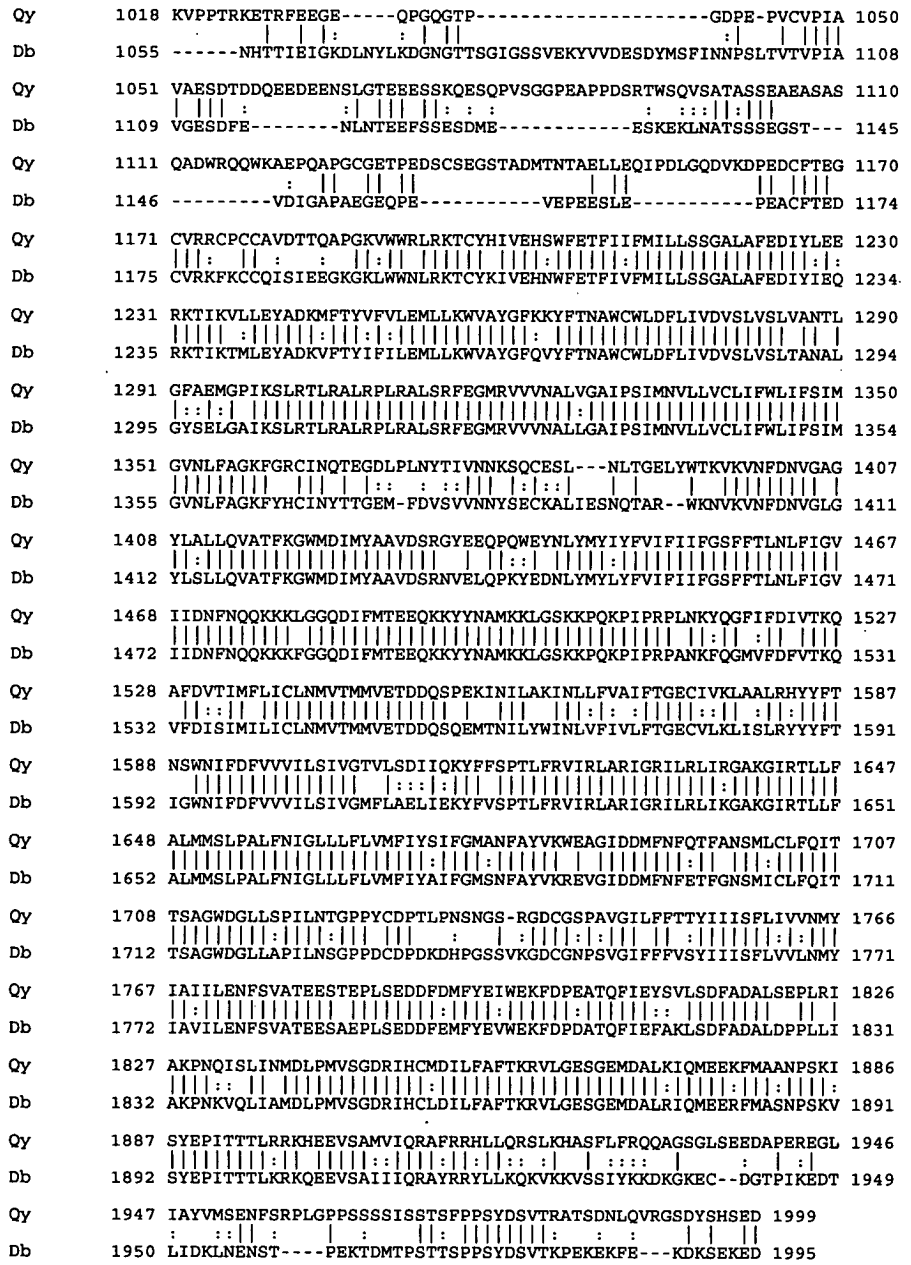
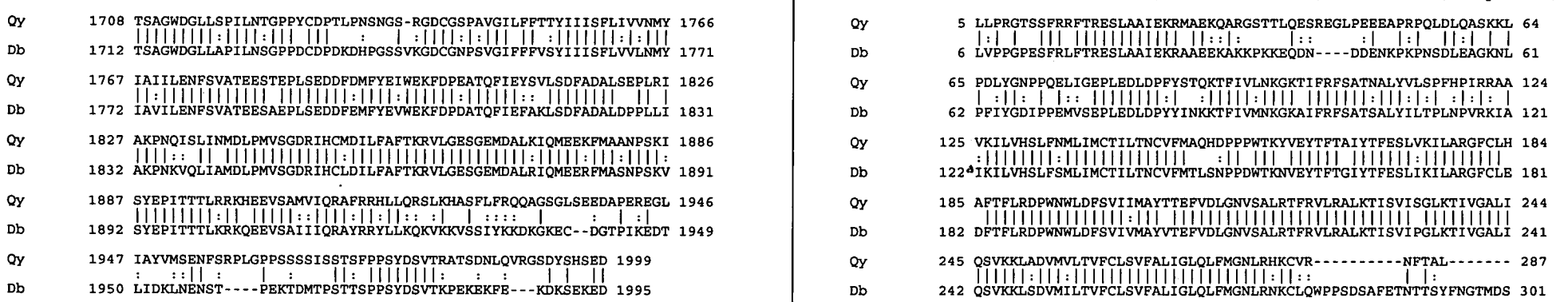
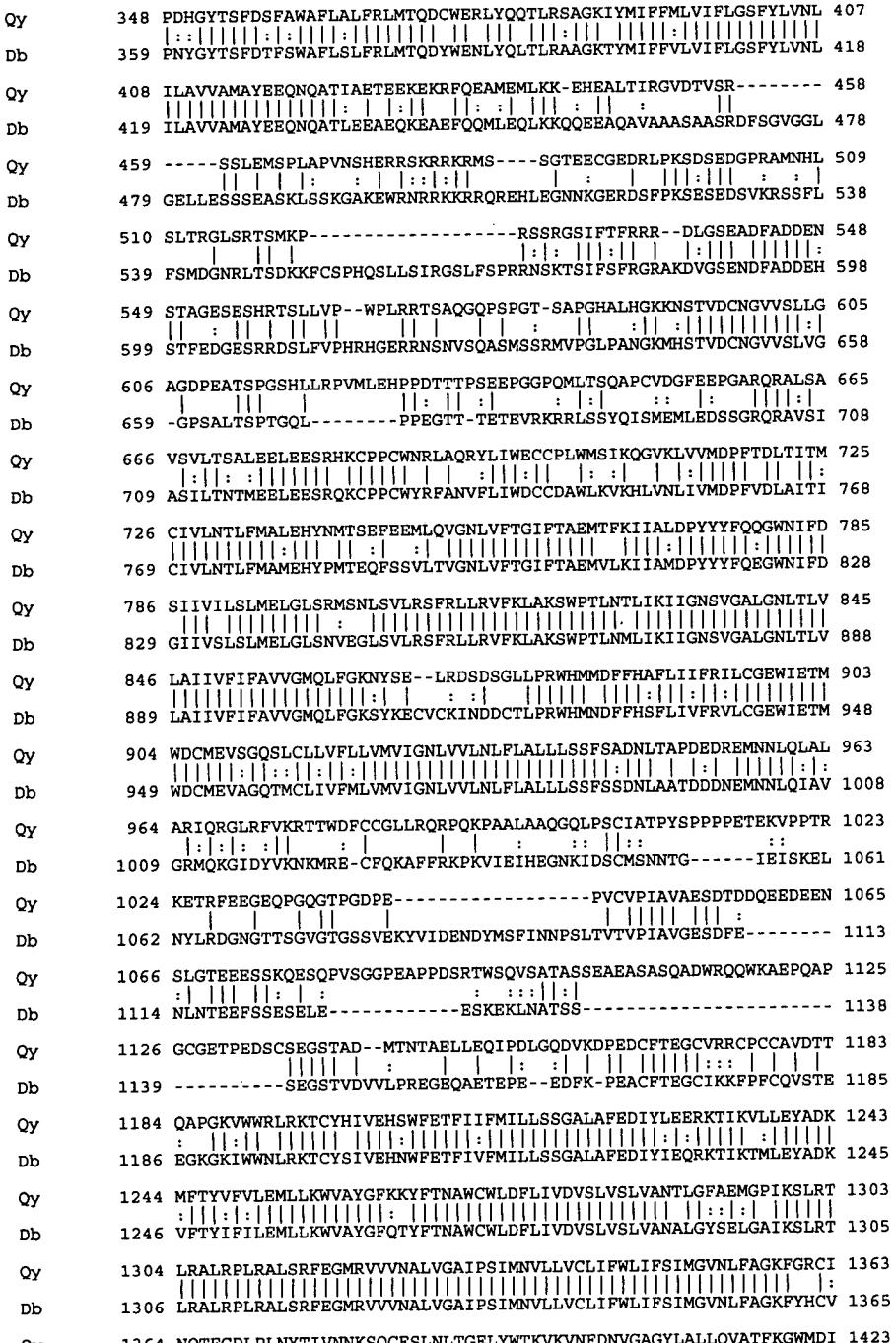


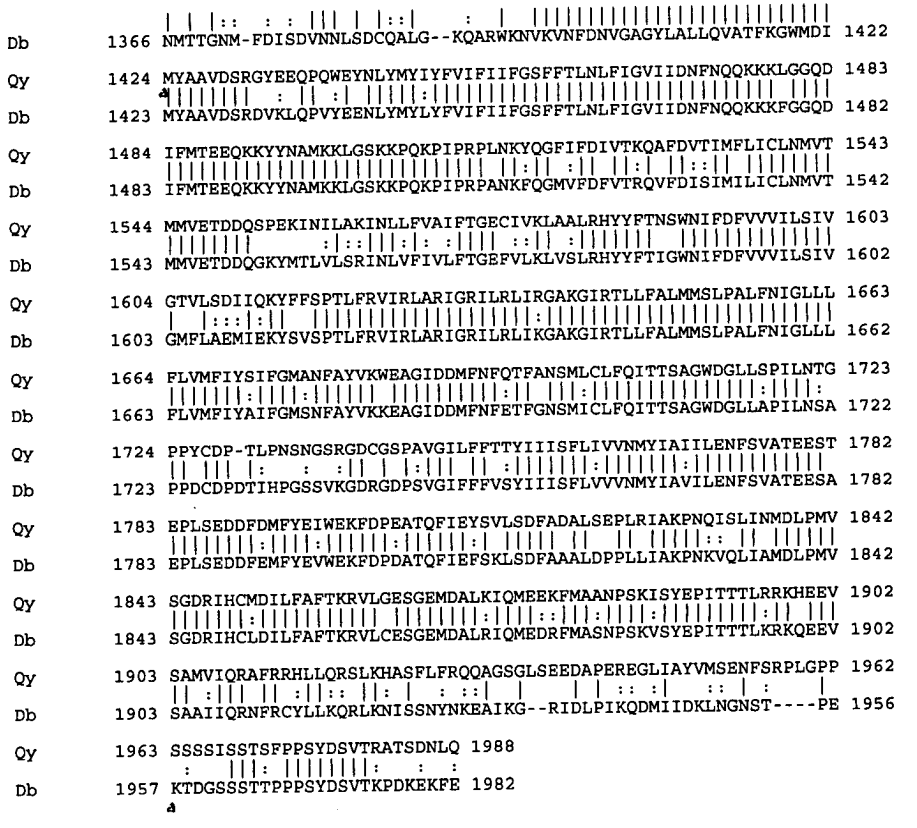
RESULT 38
ABB06027
ID ABB06027 standard; protein; 2000 AA.

XX
AC ABB06027;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN3A protein SEQ ID NO:4.
XX
KW Human; sodium channel; SCN3A; chromosome 2q24-31;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP004956.
XX
PR 13-JUN-2000; 2000JP-00177540.
PR 13-JUN-2000; 2000JP-00177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI; 2002-098066/13.
DR N-PSDB; ABL39690.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate and
PT causes of diseases and developing drugs for motor endplate disease.
XX
PS Claim 2; Page 72-81; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence represents the human sodium channel SCN3A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC studying the physiological mechanism in which excitant cells participate
CC and cause human diseases, and in developing remedies for e.g. familial
CC hypercalcaemic periodic paralysis of extremities and motor endplate
CC disease
XX
SQ Sequence 2000 AA;

Query Match 60.8%; Score 6377.5; DB 5; Length 2000;
Best Local Similarity 62.7%; Pred. No. 0;
Matches 1296; Conservative 227; Mismatches 372; Indels 171; Gaps 29;







RESULT 39
ADK81762
ID ADK81762 standard; protein; 2000 AA.
XX
AC ADK81762;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human Nav1.3 protein.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia.
XX
OS Homo sapiens.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.

DR N-PSDB; ADK81761.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Disclosure; SEQ ID NO 9096; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents human Nav1.3 protein.
XX
SQ Sequence 2000 AA;

Query Match 60.8%; Score 6377.5; DB 8; Length 2000;
Best Local Similarity 62.7%; Pred. No. 0;
Matches 1296; Conservative 227; Mismatches 372; Indels 171; Gaps 29;

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Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||||| ||::|:     |::     :|  |:|  ||:| | |
Db          6 LVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDN----DDENKPKPNSDLEAGKNL 61

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
              |:||: | |:: |||||||:|  :|||||:|||| |||||||:|||:|:| :|:|: |
Db         62 PFIYGDIPPEMVSEPLEDLDPYYINKKTFIVMNKGKAIFRFSATSALYILTPLNPVRKIA 121

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||:|||||||||||||   :|| ||| |||||| |||||||:|||||||||
Db        122 IKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 181

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||||:||| ||||||||||||||||||||||||||||| ||||||||||
Db        182 DFTFLRDPWNWLDFSVIVMAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 241

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTAL------- 287
              ||||||:|||:|||||||||||||||||||:||::         | |:
Db        242 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFNGTMDS 301

Qy        288 NGTNGSVEADGLVWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGEN 347
              |||  :|      |:    |: |  :: : :|  | ||||| |||| ||||| |:||| |
Db        302 NGTFVNVTMSTFNWKD---YIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGYICVKAGRN 358

Qy        348 PDHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNL 407
              |::||||||:|:||||:|||||||| || ||| |||:||| |||||:|||||||||||||
Db        359 PNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLVNL 418

Qy        408 ILAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKK-EHEALTIRGVDTVSR-------- 458
              |||||||||||||||: | |:||  ||: :| ||| : ||  :        ||
Db        419 ILAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGVGGL 478

Qy        459 -----SSLEMSPLAPVNSHERRSKRRKRMS----SGTEECGEDRLPKSDSEDGPRAMNHL 509
                  || | | |:   : | |::|:||       |  :   |  |||:|||  :  : |
Db        479 GELLESSSEASKLSSKGAKEWRNRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRSSFL 538

Qy        510 SLTRGLSRTSMKP------------------RSSRGSIFTFRRR--DLGSEADFADDEN 548
                  |   || |                   |:|: |||:|| |  |:||| ||||||:
Db        539 FSMDGNRLTSDKKFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEH 598

Qy        549 STAGESESHRTSLLVP--WPLRRTSAQGQPSPGT-SAPGHALHGKKNSTVDCNGVVSLLG 605
              ||  : || | || ||     || |   | |  :   ||   :|| :||||||||||:|
Db        599 STFEDGESRRDSLFVPHRHGERRNSNVSQASMSSRMVPGLPANGKMHSTVDCNGVVSLVG 658

Qy        606 AGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSA 665
              |    |||   |         ||: || :|     : |:|    ::  |:   ||||:|

Db        659 -GPSALTSPTGQL--------PPEGTT-TETEVRKRRLSSYQISMEMLEDSSGRQRAVSI 708

Qy        666 AVSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITM 725
                |:||: :|||||| |||||| | |  :|||:||  |: :|  | |:|||| || ||:
Db        709 ASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDPFVDLAITI 768

Qy        726 CIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFD 785
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db        769 CIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPYYYFQEGWNIFD 828

Qy        786 SIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLV 845
              ||| |||||||| :  |||||||||||||||||||||| ||||||||||||||||||
Db        829 GIIVSLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLV 888

Qy        846 LAIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETM 903
              |||||||||||||||||:| |   : :|   |||||| ||||:|||:||:|||||||||
Db        889 LAIIVFIFAVVGMQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETM 948

Qy        904 WDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLAL 963
              ||||||:||::||:||:|||||||||||||||||||||||:||| | |:| ||||||:|:
Db        949 WDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAV 1008

Qy        964 ARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVPPTR 1023
              |:|:|: :||   : |     | |   :   :: ||::          ::
Db       1009 GRMQKGIDYVKNKMRE-CFQKAFFRKPKVIEIHEGNKIDSCMSNNTG------IEISKEL 1061

Qy       1024 KETRFEEGEQPGQGTPGDPE-----------------PVCVPIAVAESDTDDQEEDEEN 1065
                |   |  | ||   |                   | ||||| ||| :
Db       1062 NYLRDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFE-------- 1113

Qy       1066 SLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAP 1125
              :| ||| ||: | :          :  :::||:|
Db       1114 NLNTEEFSSESELE-----------ESKEKLNATSS---------------------- 1138

Qy       1126 GCGETPEDSCSEGSTAD--MTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTT 1183
                     |||||  |  :    |  |  |:  :| | || ||||||::: | | | |
Db       1139 ----------SEGSTVDVVLPREGEQAETEPE--EDFK-PEACFTEGCIKKFPFCQVSTE 1185

Qy       1184 QAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADK 1243
              :  ||:|| |||||| ||||:||||||:||||||||||||||||:|:||||| :||||||
Db       1186 EGKGKIWWNLRKTCYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADK 1245

Qy       1244 MFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRT 1303
              :|||:|:|||||||||||: |||||||||||||||||||||||| ||::|:| ||||||
Db       1246 VFTYIPILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRT 1305

Qy       1304 LRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCI 1363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |:
Db       1306 LRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCV 1365

Qy       1364 NQTEGDLPLNYTIVNNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDI 1423
              | | |::  : : ||| | |::|    :  | |||||||||||||||||||||||||||
Db       1366 NMTTGNM-FDISDVNNLSDCQALG--KQARWKNVKVNFDNVGAGYLALLQVATFKGWMDI 1422

Qy       1424 MYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQD 1483
              |||||||  : || :| |||||:|||||||||||||||||||||||||||||| ||||
Db       1423 MYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQD 1482

Qy       1484 IFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVT 1543
              |||||||||||||||||||||||||||||| ||:|| :|| ||:| ||::|| |||||||
Db       1483 IFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVT 1542

Qy       1544 MMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIV 1603
              |||||||       :|::|||:|: :|||| ::|| :|||||||  ||||||||||||||
Db       1543 MMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGWNIFDFVVVILSIV 1602

Qy       1604 GTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLL 1663
              |  |:::|:||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GMFLAEMIEKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLL 1662

Qy       1664 FLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTG 1723
              |||||||:||||:|||||| ||||||||||:|| |||:||||||||||||:||||:
Db       1663 FLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSA 1722
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Qy       1724 PPYCDP-TLPNSNGSRGDCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEEST 1782
                 || ||| |:   :  :|| | |:||| || :|||||||:|||||||:||||||||||||
Db       1723 PPDCDPDTIHPGSSVKGDRGDPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESA 1782

Qy       1783 EPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMV 1842
                 |||||||:||||:||||||:||||||:| ||||| ||  || |||||:: || ||||||
Db       1783 EPLSEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAALDPPLLIAKPNKVQLIAMDLPMV 1842

Qy       1843 SGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEV 1902
                 |||||||:|||||||||||| ||||||||:||||::|||:||||:|||||||||:|| |||
Db       1843 SGDRIHCLDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQEEV 1902

Qy       1903 SAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPP 1962
                 || :||| || :||:: ||: |  : ::|  |     | | :: :|   :: | :    |
Db       1903 SAAIIQRNFRCYLLKQRLKNISSNYNKEAIKG--RIDLPIKQDMIIDKLNGNST----PE 1956

Qy       1963 SSSSISSTSFPPSYDSVTRATSDNLQ 1988
                :   |||: ||||||||:   :  :
Db       1957 KTDGSSSTTPPPSYDSVTKPDKEKFE 1982
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RESULT 40
ADP79545
ID ADP79545 standard; protein; 2000 AA.
XX
AC ADP79545;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human sodium III channel SCN3A splice variant.
XX
KW Human; sodium III channel; SCN3A; antiarrhythmic; analgesic.
XX
OS Homo sapiens.
XX
PN WO2004050857-A2.
XX
PD 17-JUN-2004.
XX
PF 04-DEC-2003; 2003WO-US038796.
XX
PR 04-DEC-2002; 2002US-0431794P.
XX
PA (EURO-) EUROCELTIQUE SA.
XX
PI Kammesheidt A, Hodges D;
XX
DR WPI; 2004-450725/42.
DR N-PSDB; ADP79544.
DR GENBANK; AF225987.
XX
PT New human sodium III channel, useful in treating cardiac arrhythmias,
PT herpes virus infection, diabetes mellitus, or vasculitis.
XX
PS Example 1; SEQ ID NO 6; 101pp; English.
XX
CC The present sequence is that of a previously identified splice variant of
CC the human sodium III channel polypeptide. The sequence differs from a
CC newly identified splice variant ADP79541 of the sodium III channel,
CC denoted hNaIII18, by 12 amino acids out of 2000. The invention provides:
CC hNaIII18 proteins and their fragments and derivatives; hNaIII18-encoding
CC nucleic acids and their fragments, including primers, probes, and
CC hNaIII18 regulatory sequences; hNaIII18-specific antibodies; and methods
CC of using these materials to detect the presence of hNaIII18 proteins or
CC nucleic acids. The invention also provides an assay method for screening
CC to identify selective modulators of hNaIII18 expression or activity.
CC These may be useful for treatment of conditions associated with sodium
CC channel over- or under-expression, e.g. for treatment of cardiac
CC arrhythmia, neuronal disorders, nociceptive pain-related diseases and
CC neuropathic pain-related diseases, e.g. pain from peripheral nerve
CC trauma, herpes virus infection, diabetes mellitus, causalgia, plexus
CC avulsion, neuroma, limb amputation or vasculitis.

XX
SQ Sequence 2000 AA;

Query Match 60.8%; Score 6377.5; DB 8; Length 2000;
Best Local Similarity 62.7%; Pred. No. 0;
Matches 1296; Conservative 227; Mismatches 372; Indels 171; Gaps 29;

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Qy          5 LLPRGTSSFRRFTRESLAAIEKRMAEKQARGSTTLQESREGLPEEEAPRPQLDLQASKKL 64
              |:| |  ||| |||||||||||| ||::|:     |::     :|  |:|  ||:| | |
Db          6 LVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDN----DDENKPKPNSDLEAGKNL 61

Qy         65 PDLYGNPPQELIGEPLEDLDPFYSTQKTFIVLNKGKTIFRFSATNALYVLSPFHPIRRAA 124
               | :||: | |:: ||||||||:|  :|||||:|||| |||||||:|||:|:| :|:|: |
Db         62 PFIYGDIPPEMVSEPLEDLDPYYINKKTFIVMNKGKAIFRFSATSALYILTPLNPVRKIA 121

Qy        125 VKILVHSLFNMLIMCTILTNCVFMAQHDPPPWTKYVEYTFTAIYTFESLVKILARGFCLH 184
              :|||||||:|||||||||||||    :|| ||| |||||| |||||||:|||||||||
Db        122 IKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLE 181

Qy        185 AFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSALRTFRVLRALKTISVISGLKTIVGALI 244
              |||||||||||||||:||| |||||||||||||||||||||||||||| ||||||||||
Db        182 DFTFLRDPWNWLDFSVIVMAYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALI 241

Qy        245 QSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVR----------NFTAL------- 287
              ||||||:|||:|||||||||||||||||||:||::          | |:
Db        242 QSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFNGTMDS 301

Qy        288 NGTNGSVEADGLVWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGEN 347
              ||| :|     |:    |: |  :: : :|  | ||||| |||| ||||| |:||| |
Db        302 NGTFVNVTMSTFNWKD---YIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGYICVKAGRN 358

Qy        348 PDHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAGKIYMIFFMLVIFLGSFYLVNL 407
              |::|||||:|:||||:|||||||| || ||| |||:||| |||||:|||||||||||||
Db        359 PNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLVNL 418

Qy        408 ILAVVAMAYEEQNQATIAETEEKEKRFQEAMEMLKK-EHEALTIRGVDTVSR-------- 458
              |||||||||||||||: | |:||  ||: :| ||| : ||  :       ||
Db        419 ILAVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGVGGL 478

Qy        459 -----SSLEMSPLAPVNSHERRSKRRKRMS----SGTEECGEDRLPKSDSEDGPRAMNHL 509
                  || | | |:   : | |::|:||       |  :   |  |||:|||  :  : |
Db        479 GELLESSSEASKLSSKGAKEWRNRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRSSFL 538

Qy        510 SLTRGLSRTSMKP------------------RSSRGSIFTFRRR--DLGSEADFADDEN 548
                  |   || |                  |:|: |||:|| |  |:||| ||||||:
Db        539 FSMDGNRLTSDKKFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEH 598

Qy        549 STAGESESHRTSLLVP--WPLRRTSAQGQPSPGT-SAPGHALHGKKNSTVDCNGVVSLLG 605
              ||  : || | || ||      || |   | |  :   ||   :|| :|||||||||||:|
Db        599 STFEDGESRRDSLFVPHRHGERRNSNVSQASMSSRMVPGLPANGKMHSTVDCNGVVSLVG 658

Qy        606 AGDPEATSPGSHLLRPVMLEHPPDTTTPSEEPGGPQMLTSQAPCVDGFEEPGARQRALSA 665
              |   |||  |        ||: || :|     : |:|    ::  |:   ||||:|
Db        659 -GPSALTSPTGQL--------PPEGTT-TETEVRKRRLSSYQISMEMLEDSSGRQRAVSI 708

Qy        666 VSVLTSALEELEESRHKCPPCWNRLAQRYLIWECCPLWMSIKQGVKLVVMDPFTDLTITM 725
              |:||: :||||||| |||||| | |  :|||:||  |: :|  | |:||||| || ||:
Db        709 ASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDPFVDLAITI 768

Qy        726 CIVLNTLFMALEHYNMTSEFEEMLQVGNLVFTGIFTAEMTFKIIALDPYYYFQQGWNIFD 785
              |||||||||:||| || :|  :| |||||||||||||  ||||:|||||||:||||||
Db        769 CIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPYYYFQEGWNIFD 828

Qy        786 SIIVILSLMELGLSRMSNLSVLRSFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTLV 845
              ||| |||||||||  :  |||||||||||||||||||||| ||||||||||||||||||
Db        829 GIIVSLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLV 888

Qy        846 LAIIVFIFAVVGMQLFGKNYSE--LRDSDSGLLPRWHMMDFFHAFLIIFRILCGEWIETM 903
              |||||||||||||||||:|  |   : :|   |||||| ||||:|||:|||||||||
Db        889 LAIIVFIFAVVGMQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETM 948

Qy        904 WDCMEVSGQSLCLLVFLLVMVIGNLVVLNLFLALLLSSFSADNLTAPDEDREMNNLQLAL 963
              ||||||:||::||:||:|||||||||||||||||||:||| | |:| ||||||:|:
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Db        949 WDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAV 1008

Qy        964 ARIQRGLRFVKRTTWDFCCGLLRQRPQKPAALAAQGQLPSCIATPYSPPPPETEKVPPTR 1023

Db       1009 GRMQKGIDYVKNKMRE-CFQKAFFRKPKVIEIHEGNKIDSCMSNNTG------IEISKEL 1061

Qy       1024 KETRFEEGEQPGQGTPGDPE-----------------PVCVPIAVAESDTDDQEEDEEN 1065

Db       1062 NYLRDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFE-------- 1113

Qy       1066 SLGTEEESSKQESQPVSGGPEAPPDSRTWSQVSATASSEAEASASQADWRQQWKAEPQAP 1125

Db       1114 NLNTEEFSSESELE------------ESKEKLNATSS---------------------- 1138

Qy       1126 GCGETPEDSCSEGSTAD--MTNTAELLEQIPDLGQDVKDPEDCFTEGCVRRCPCCAVDTT 1183

Db       1139 ----------SEGSTVDVVLPREGEQAETEPE--EDFK-PEACFTEGCIKKPPFCQVSTE 1185

Qy       1184 QAPGKVWWRLRKTCYHIVEHSWFETFIIFMILLSSGALAFEDIYLEERKTIKVLLEYADK 1243

Db       1186 EGKGKIWWNLRKTCYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADK 1245

Qy       1244 MFTYVFVLEMLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRT 1303

Db       1246 VFTYIFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRT 1305

Qy       1304 LRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCI 1363

Db       1306 LRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCV 1365

Qy       1364 NQTEGDLPLNYTIVNNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGWMDI 1423

Db       1366 NMTTGNM-FDISDVNNLSDCQALG--KQARWKNVKVNFDNVGAGYLALLQVATFKGWMDI 1422

Qy       1424 MYAAVDSRGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQD 1483

Db       1423 MYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQD 1482

Qy       1484 IFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVT 1543

Db       1483 IFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVT 1542

Qy       1544 MMVETDDQSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIV 1603

Db       1543 MMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGWNIFDFVVVILSIV 1602

Qy       1604 GTVLSDIIQKYFFSPTLFRVIRLARIGRILRLIRGAKGIRTLLFALMMSLPALFNIGLLL 1663

Db       1603 GMFLAEMIEKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLL 1662

Qy       1664 FLVMFIYSIFGMANFAYVKWEAGIDDMFNFQTFANSMLCLFQITTSAGWDGLLSPILNTG 1723

Db       1663 FLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSA 1722

Qy       1724 PPYCDP-TLPNSNGSRGDCGSPAVGILFFTTYIIISFLIVVNMYIAIILENFSVATEEST 1782

Db       1723 PPDCDPDTIHPGSSVKGDRGDPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESA 1782

Qy       1783 EPLSEDDFDMFYEIWEKFDPEATQFIEYSVLSDFADALSEPLRIAKPNQISLINMDLPMV 1842

Db       1783 EPLSEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAALDPPLLIAKPNKVQLIAMDLPMV 1842

Qy       1843 SGDRIHCMDILFAFTKRVLGESGEMDALKIQMEEKFMAANPSKISYEPITTTLRRKHEEV 1902

Db       1843 SGDRIHCLDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQEEV 1902

Qy       1903 SAMVIQRAFRRHLLQRSLKHASFLFRQQAGSGLSEEDAPEREGLIAYVMSENFSRPLGPP 1962

Db       1903 SAAIIQRNFRCYLLKQRLKNISSNYNKEAIKG--RIDLPIKQDMIIDKLNGNST----PE 1956

Qy       1963 SSSSISSTSFPPSYDSVTRATSDNLQ 1988

Db       1957 KTDGSSSTTPPPSYDSVTKPDKEKFE 1982
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